

SEQUENCE LISTING

<110> Kalyanaraman Ramnarayan
Edward T. Maggio
P. Patrick Hess

<120> Use of Computationally Derived Protein
Structures of Genetic Polymorphisms in Pharmacogenomics for
Drug Design and Clinical Applications

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Peptide

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<307> 1998-06-23

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 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
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 Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ttt atc aaa gta aga cag tat gat caa ata ctc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile
 50 55 60
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 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80
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 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
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- 3 -

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Ile	Arg	Tyr	Gln 245	Tyr	Asn	Val	Leu	Pro	Gln 250	Gly	Trp	Lys	Gly 255	Ser	Pro	
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Ala	Ile	Phe	Gln 260	Ser	Ser	Met	Thr	Lys 265	Ile	Leu	Glu	Pro	Phe 270	Arg	Lys	
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Gln	Asn	Pro 275	Asp	Ile	Val	Ile	Tyr 280	Gln	Tyr	Met	Asp	Asp 285	Leu	Tyr	Val	
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Ser	Ser 290	Asp	Leu	Glu	Ile	Gly 295	Gln	His	Arg	Thr	Lys 300	Ile	Glu	Glu	Leu	
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Arg 305	Gln	His	Leu	Leu	Arg 310	Trp	Gly	Leu	Thr	Thr 315	Pro	Asp	Lys	Lys	His 320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro 325	Phe	Leu	Trp	Met	Gly 330	Tyr	Glu	Leu	His	Pro 335	Asp	
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gar	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val 340	Gln	Pro	Ile	Val	Leu 345	Pro	Glu	Lys	Asp	Ser 350	Trp	Thr	
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	caa	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	

00011-50550260

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355          360          365
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<210> 9
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

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1          5          10          15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
          20          25          30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
          35          40          45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
          50          55          60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
          65          70          75

cct gtc aac ata atw gga aga aat ctg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Xaa Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
          85          90          95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
          100          105          110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
          115          120          125

aaa ata aaa gca tta ata gaa att tgt aca gag atg gag aag gaa ggg      432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
          130          135          140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
          145          150          155          160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
          165          170          175

aga gaa ctt aat aag aaa act caa gay ttc tgg gaa gtt car tta gga      576

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Ile	Pro	His 195	Pro	Ala	Gly	Leu	Lys 200	Lys	Lys	Lys	Ser	Val 205	Thr	Val	Leu		
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg		672
Asp	Val	Gly	Asp	Ala	Tyr	Phe 215	Ser	Val	Pro	Leu	Asp 220	Lys	Asp	Phe	Arg		
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Lys	Tyr	Thr	Ala	Phe	Thr 230	Ile	Pro	Ser	Val	Asn 235	Asn	Glu	Thr	Pro	Gly 240		
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Ile	Arg	Tyr	Gln	Tyr 245	Asn	Val	Leu	Pro	Gln	Gly 250	Trp	Lys	Gly	Ser	Pro 255		
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Ala	Ile	Phe	Gln 260	Ser	Ser	Met	Thr	Lys 265	Ile	Leu	Glu	Pro	Phe 270	Arg	Lys		
caa	aat	cca	gaa	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta		864
Gln	Asn	Pro 275	Glu	Ile	Val	Ile	Tyr 280	Gln	Tyr	Met	Asp	Asp 285	Leu	Tyr	Val		
gga	tcw	gac	tta	gaa	ata	ggg	caa	cat	aga	ata	aaa	ata	gag	gaa	ctg		912
Gly	Xaa	Asp	Leu	Glu	Ile	Gly 295	Gln	His	Arg	Ile	Lys 300	Ile	Glu	Glu	Leu		
aga	cag	cat	ctg	tta	agg	tgg	ggg	ttt	acc	aca	cca	gac	aaa	aaa	cat		960
Arg	Gln	His	Leu	Leu	Arg 310	Trp	Gly	Phe	Thr	Thr 315	Pro	Asp	Lys	Lys	His 320		
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggk	tat	gaa	ctc	cat	cct	gat		1008
Gln	Lys	Glu	Pro	Pro 325	Phe	Leu	Trp	Met	Xaa 330	Tyr	Glu	Leu	His	Pro 335	Asp		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gay	agc	tgg	act		1056
Lys	Trp	Thr	Val 340	Gln	Pro	Ile	Val	Leu 345	Pro	Glu	Lys	Asp	Ser 350	Trp	Thr		
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	cag		1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val 360	Gly	Lys	Leu	Asn	Trp 365	Ala	Ser	Gln		
atc	tac	cca	ggg														1116
Ile	Tyr	Pro	Gly 370														

<210> 10
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 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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ggg Gly	caa Gln	ata Ile	aag Lys 20	gaa Glu	gct Ala	yta Xaa	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96
tta Leu	gaa Glu	gaa Glu 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atw Xaa	ata Ile	ggg Gly	144
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	gta Val	ccc Pro	ata Ile	192
gaa Glu 65	atc Ile	tgt Cys	gga Gly	caa Gln	aaa Lys 70	gct Ala	ata Ile	agt Ser	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aat Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	atg Met 90	act Thr	cag Gln	att Ile	ggt Gly	tgc Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	cct Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	taa *	aag Lys	336
cca Pro	gga Gly	atg Met	gat Asp 115	ggc Gly	cca Pro	aga Arg	gtt Val	aaa Lys 120	caa Gln	tgg Trp	cca Pro	ttg Leu	aca Thr 125	gaa Glu	gaa Glu	384
aaa Lys	ata Ile	aaa Lys 130	gca Ala	tta Leu	gta Val	gaa Glu	atc Ile 135	tgt Cys	aca Thr	gaa Glu	atg Met	gaa Glu 140	aag Lys	gaa Glu	ggg Gly	432
aaa Lys	att Ile 145	tca Ser	aaa Lys	att Ile	ggg Gly	cct Pro 150	gaa Glu	aat Asn	cca Pro	tac Tyr	aat Asn 155	act Thr	cca Pro	gta Val	ttt Phe	480
gcc Ala 160	ata Ile	aag Lys	aaa Lys	aaa Lys	ggc Gly 165	agt Ser	aac Asn	aga Arg	tgg Trp	aga Arg 170	aaa Lys	tta Leu	gta Val	gat Asp	ttc Phe 175	528
aga Arg	gaa Glu	ctt Leu	aat Asn	aag Lys 180	aaa Lys	act Thr	caa Gln	gac Asp	ttc Phe 185	tgg Trp	gaa Glu	gtt Val	caa Gln	tta Leu 190	gga Gly	576
ata Ile	cca Pro	cat His	ccc Pro 195	gca Ala	ggg Gly	cta Leu	aaa Lys	aag Lys 200	aaa Lys	aaa Lys	tca Ser	gta Val	aca Thr 205	gta Val	ctg Leu	624
gat Asp	gtg Val	ggt Gly 210	gat Asp	gca Ala	tat Tyr	ttt Phe	tca Ser 215	gtt Val	ccc Pro	tta Leu	gat Asp	aaa Lys 220	gaa Glu	ttc Phe	agg Arg	672
aag Lys	tat Tyr 225	act Thr	gca Ala	ttt Phe	acc Thr	ata Ile 230	cct Pro	agt Ser	aca Thr	aac Asn	aat Asn 235	gag Glu	aca Thr	cca Pro	ggg Gly	720
att Ile 240	aga Arg	tat Tyr	cag Gln	tac Tyr	aat Asn 245	gtg Val	ctt Leu	ccm Xaa	caa Gln	gga Gly 250	tgg Trp	aaa Lys	ggg Gly	tca Ser	cca Pro 255	768
gca Ala	ata Ile	ttc Phe	caa Gln	agt Ser 260	agc Ser	atg Met	aca Thr	aaa Lys	atc Ile 265	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816

caa aat cca gac wtr gtt atc tat caa tac atg gat gat ttg tat gta	864
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275 280 285	
agc tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa cta	912
Ser Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga tta acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His	
305 310 315	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
320 325 330 335	
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa	1104
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ggg caa cta aaa raa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Xaa Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata gtg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val	
35 40 45	
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta ccc ata	192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile	
50 55 60	
gag atc tgt ggg cat aaa att ata ggt aca gta tta ata gga cct acc	240
Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gcc aac gta att gga aga aat ctg atg act cag ctt ggt tgc act	288
Pro Ala Asn Val Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr	

85										90										95										
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Leu	Asn	Phe	Pro	Ile	Ser	Xaa	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys															
			100					105					110																	
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu															
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Ala	Ile	Lys	Lys	Lys	Asn	Ser	Thr	Arg	Trp	Arg	Lys	Leu	Val	Asp	Phe															
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Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Ile	Gln	Leu	Gly															
			180					185					190																	
ata	cca	cat	cct	gca	ggg	tta	aaa	aag	aac	aaa	tca	gta	aca	gta	ctg	624														
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu															
		195				200						205																		
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Ala	Ile	Phe	Gln	Asp	Ser	Met	Thr	Lys	Ile	Leu	Asp	Pro	Phe	Arg	Lys															
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Lys	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val															
		275				280					285																			
gga	tct	gac	yta	gaa	ata	gag	cag	cat	aga	gca	aaa	ata	gag	gaa	ctg	912														
Gly	Ser	Asp	Xaa	Glu	Ile	Glu	Gln	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu															
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Arg	Glu	Tyr	Leu	Leu	Lys	Trp	Gly	Phe	Phe	Thr	Pro	Glu	Gln	Lys	His															
	305				310				315						320															
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggc	tat	gaa	ctc	cat	cct	gat	1008														
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp															
				325					330					335																
aaa	tgg	aca	gtg	cag	cct	ata	gtg	ctg	cca	gaa	aag	gac	agc	tgg	act	1056														
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr															
			340					345					350																	
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att tac cca ggg
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1116

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 ggg caa cta aag gaa gcc cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30
 cta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ttt atc aaa gta agg cag tat gat car ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60
 gag atc tgc ggg tat aaa gct gtg ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly Tyr Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80
 cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa gac ggt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat caa gac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asp Phe Arg	
210 215 220	
aag tat act gca ttc act ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac atg gtt atc tat caa tat atg gat gat ttg tat gta	864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
ggc tct gac tta gaa aya ggg cag cat aga rca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Xaa Gly Gln His Arg Xaa Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata atg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Met Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag cta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca ggg	1116
Ile Tyr Ala Gly	
370	

<210> 13
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 <213> Human Immunodeficiency Virus (HIV)
 <220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease
 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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ggg caa cta arg gaa gct cta ata gat aca gga gca gat gat aca gta Gly Gln Leu Xaa Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac ata gat ttg cca gga aga tgg aga cca aga atg ata ggg Leu Glu Asp Ile Asp Leu Pro Gly Arg Trp Arg Pro Arg Met Ile Gly 35 40 45	144
gga att gga ggt ttt gtc aaa gta aag cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa ata tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct acg Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag att ggg tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aag ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aag aaa aac agt act aga tgg aga aaa tta gta gat ttt Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
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ata ccg cat ccc gca ggg tta ara aag aaa aga tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Xaa Lys Lys Arg Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gcc ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816

	260	265	270	
caa aat cca grc ata gtt atc gtt caa tac gtg gat gat ttg tat gta				864
Gln Asn Pro Xaa Ile Val Ile Val Gln Tyr Val Asp Asp Leu Tyr Val				
	275	280	285	
ggg tct gac tta gaa ata ggg caa cat aga gca aaa ata gag gag ttg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu				
	290	295	300	
aga gaa cat ctg ttg agg tgg gga tty ttc aca cca gac gaa aaa cat				960
Arg Glu His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Glu Lys His				
	305	310	315	320
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cac cct gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp				
	325		330	335
aaa tgg acc gta cag cct ata aat ttg cca gaa aaa gac agc tgg act				1056
Lys Trp Thr Val Gln Pro Ile Asn Leu Pro Glu Lys Asp Ser Trp Thr				
	340	345	350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag				1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
	355	360	365	
att tac tca ggg				1116
Ile Tyr Ser Gly				
	370			
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	1	5	10	15
ggg caa gta agg gaa gct cta tta gat aca gga gca gat gat aca gta				96
Gly Gln Val Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val				
	20	25	30	
tta gaa gaa atg aat ttg cca gga aaa tgg aag cca aaa atg ata ggg				144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly				
	35	40	45	
gga att ggg ggc ttt atc aaa gta aga cag tat gat caa ata ccc ata				192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile				
	50	55	60	
gaa atc tgt gga cat aaa gct ata ggg aca gtg tta ata gga cct aca				240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr				
	65	70	75	80
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act				288

gtc aat gac ata caa aag tta gtg gga aaa tta aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca ggg	1116
Ile Tyr Ala Gly	
370	
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1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta kaa gaa atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Xaa Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta tcc wta	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Xaa	
50 55 60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tat aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttg gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	

aga gaa ctt aat aag aaa act caa gac ttc tgg gar gtt caa tta gga	576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg	
210 215 220	
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Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttt caa agy agc atg ata aga aty tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Xaa Ser Met Ile Arg Xaa Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gaa ata gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gat tta gaa ata gaa cag cat aga gca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Ala Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg tta agg tgg gga ttt acc aca cca gay aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggk tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag ttr gtg gga aaa ttr aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Xaa Val Gly Lys Xaa Asn Trp Ala Ser Gln	
355 360 365	
att tac tca ggg	1116
Ile Tyr Ser Gly	
370	

<210> 16

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<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (0)...(297)

<223> HIV Protease

<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
275				280				285								
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	rca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Xaa	Lys	Ile	Glu	Glu	Leu	
290				295				300								
agg	caa	cat	ctg	ttg	aag	tgg	gga	ttt	acc	aca	cca	gac	aaa	aaa	cat	960
Arg	Gln	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
305				310				315				320				
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggt	tat	gaa	ctc	cat	cca	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325				330				335				
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	caa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Gln	Lys	Asp	Ser	Trp	Thr	
				340				345				350				
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
				355				360				365				
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Ile	Tyr	Pro	Gly													
370																

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<210> 17
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<212> DNA
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<220>
<221> CDS
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<223> HIV Protease

<221> CDS
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<223> Portion of HIV Reverse Transcriptase
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Xaa	Val	Thr	Ile	Lys	Val	Gly	
1				5					10					15		
ggg caa cta aag gaa gcc cta ata gat aca gga gca gat gat aca gtg																96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Ile	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg																144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Leu	Ile	Gly	
		35					40					45				
gga att gga ggt ttt atc aaa gta aga cag tat gat cag rta ccc ata																192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Xaa	Pro	Ile	
	50					55					60					
gaa atc tgt gga cat aaa gct gta ggt tca gtg tta gta gga cct aca																240
Glu	Ile	Cys	Gly	His	Lys	Ala	Val	Gly	Ser	Val	Leu	Val	Gly	Pro	Thr	
65					70					75					80	
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act																288

Pro	Ala	Asn	Ile	Ile 85	Gly	Arg	Asn	Leu	Leu 90	Thr	Gln	Ile	Gly	Cys 95	Thr	
cta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	aaa Lys	gaa Glu	384
aaa Lys	ata Ile 130	gaa Glu	gca Ala	tta Leu	gta Val	gaa Glu 135	atc Ile	tgt Cys	gca Ala	gaa Glu	ctg Leu 140	gaa Glu	gag Glu	gca Ala	ggg Gly	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aar Lys	aag Lys 165	aac Asn	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aac Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	ggg Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggg Gly	gat Asp	gca Ala	tat Tyr	ttc Phe 215	tca Ser	att Ile	ccc Pro	tta Leu	gat Asp 220	aag Lys	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	aca Thr 230	ata Ile	cct Pro	agy Xaa	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cma Xaa 250	cag Gln	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	cag Gln 260	tgt Cys	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gat Asp	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	ggg Gly 295	car Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	yat Xaa	ctg Leu	tgg Trp	aag Lys 310	tgg Trp	gga Gly	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gag Glu	aat Asn	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	cwt Xaa	tgg Trp	atg Met	ggg Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val	ctg Leu 345	cca Pro	gaa Glu	aag Lys	gac Asp	agc Ser	tgg Trp	act Thr	1056

[illegible]

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<220>
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<222> (0)...(297)
<223> HIV Protease

<221> CDS
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<223> Portion of HIV Reverse Transcriptase
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[illegible]

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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
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Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Leu	Glu	Lys	Glu	Gly	
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	cct	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggt	gat	gca	tat	ttt	tca	ata	ccc	tta	gat	gaa	gaa	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Ile	Pro	Leu	Asp	Glu	Glu	Phe	Arg	
	210					215					220					
aag	tat	act	gca	ttt	acc	ata	cct	agt	cca	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Pro	Asn	Asn	Glu	Thr	Pro	Gly	
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttt	caa	tgt	agt	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
gaa	aat	cca	gat	ata	gtt	atc	tac	caa	tac	atg	gat	gac	tta	tat	gta	864
Glu	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
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Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
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Arg	Gln	Tyr	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
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Gln	Gln	Glu	Pro	Pro	Phe	Arg	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325				330						335		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			

[illegible]

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<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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ggg caa cta aag gag gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gac ata gat ttg cca gga agr tgg aaa cca aaa atg ata ggg Leu Glu Asp Ile Asp Leu Pro Gly Xaa Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa ata tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cgg att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Arg Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttt Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
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ata ccg cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aar gay ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aag tat act gcc ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc cta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816

	260	265	270	
caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta				864
Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val				
	275	280	285	
ggg tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu				
	290	295	300	
aga gaa cat ctg ttg agg tgg gga ttt acc acc cca gac aaa aaa cat				960
Arg Glu His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His				
	305	310	315	320
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp				
	325	330	335	
aaa tgg acc gtr cag cct ata gag ctg cca gaa aaa gac agc tgg act				1056
Lys Trp Thr Xaa Gln Pro Ile Glu Leu Pro Glu Lys Asp Ser Trp Thr				
	340	345	350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag				1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
	355	360	365	
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Ile Tyr Pro Gly				
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	1	5	10	15
ggg caa cta aag gaa gct cta ata gat aca gga gca gat gat aca gta				96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val				
	20	25	30	
tta gaa gac ata aat ttg cca gga aga tgg aaa cca aaa tta ata ggg				144
Leu Glu Asp Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly				
	35	40	45	
gga att gga ggt ttt gtc aga gtg aaa cag tat gat cag ata ccc ata				192
Gly Ile Gly Gly Phe Val Arg Val Lys Gln Tyr Asp Gln Ile Pro Ile				
	50	55	60	
gaa att tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca				240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr				
	65	70	75	80
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act				288

Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aga	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Arg	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	aca	gaa	atc	tgt	wca	gag	atg	gaa	aag	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Thr	Glu	Ile	Cys	Xaa	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aac	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcy	ata	cac	aag	aaa	aat	agt	aat	aga	tgg	aga	aaa	gta	gta	gat	ttc	528
Xaa	Ile	His	Lys	Lys	Asn	Ser	Asn	Arg	Trp	Arg	Lys	Val	Val	Asp	Phe	
				165					170					175		
agg	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	gga	tta	aaa	aag	aac	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aag	gat	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210				215						220					
aag	tat	act	gcg	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
atc	aga	tac	cag	tac	aat	gtg	ctt	cca	caa	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aga	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Arg	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gaa	ata	gtt	atc	tgt	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Glu	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	aak	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Xaa	Glu	Leu	
	290					295					300					
aga	saa	cat	ctg	ttg	agg	tgg	gga	ttt	ttc	aca	cca	gac	caa	aaa	cat	960
Arg	Xaa	His	Leu	Leu	Arg	Trp	Gly	Phe	Phe	Thr	Pro	Asp	Gln	Lys	His	
	305				310					315					320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aar	gac	agt	tgg	acw	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Xaa	
			340					345					350			

agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca gga tta aaa aag aac aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gat ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gcg ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
atc aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aga atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gaa ata gtt atc tgt caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Glu Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata aak gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Xaa Glu Leu	
290 295 300	
aga saa cat ctg ttg agg tgg gga ttt ttc aca cca gac caa aaa cat	960
Arg Xaa His Leu Leu Arg Trp Gly Phe Phe Thr Pro Asp Gln Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aar gac agt tgg acw	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Xaa	
340 345 350	
gty aat gac ata cag aaa tta gtk gga aaa ttg aat tgg gca agt caa	1104
Xaa Asn Asp Ile Gln Lys Leu Xaa Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac cca ggg	1116
Ile Tyr Pro Gly	
370	

<210> 25

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>

<221> CDS

<222> (0)...(297)

<223> HIV Protease

<221> CDS

<222> (298)...(1116)

<223> Portion of HIV Reverse Transcriptase

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gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	290	295	300	912	
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	305	310	315	320	960
cag aaa gaa cct cca ttc ctc tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	325	330	335	1008	
aaa tgg aca gtt cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	340	345	350	1056	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	355	360	365	1104	
att tac cca ggg Ile Tyr Pro Gly	370			1116	
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ggg caa cta ata gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	20	25	30		96
tta gaa gaa ata aat tta cca gga aga tgg aaa cca aga atg ata ggg Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Arg Met Ile Gly	35	40	45		144
gga att gga ggt ttt gtc aaa gta aga cag tat gat cag gta cct atc Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Val Pro Ile	50	55	60		192
gaa atc tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr	65	70	75	80	240
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act					288

Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Met	Thr	Gln	Ile	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aaa	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aga	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Arg	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	ytg	gaa	gag	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Xaa	Glu	Glu	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	ata	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	
	145				150					155					160	
gcc	ata	aag	aag	aaa	nnn	agt	ggg	aga	tgg	aga	aaa	ata	gta	gat	ttt	528
Ala	Ile	Lys	Lys	Lys	Xaa	Ser	Gly	Arg	Trp	Arg	Lys	Ile	Val	Asp	Phe	
				165				170						175		
aga	gaa	ctt	aat	aag	aga	act	caa	gat	ttc	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aac	aag	tca	gta	aca	att	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Ile	Leu	
		195				200						205				
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aag	gaa	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg	
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Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245					250						255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	cag	tac	gtg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280				285					
gga	tct	gat	tta	gaa	ata	ggg	gag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Glu	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	car	cat	ctg	tta	arg	tgg	gga	ttt	ttc	aca	cca	gaa	caa	aaa	cat	960
Arg	Gln	His	Leu	Leu	Xaa	Trp	Gly	Phe	Phe	Thr	Pro	Glu	Gln	Lys	His	
	305				310					315					320	
cag	aaa	gaa	cct	ccm	ttc	cak	tgg	atg	ggg	tat	gaa	ctc	cay	cct	gat	1008
Gln	Lys	Glu	Pro	Xaa	Phe	Xaa	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
			325					330						335		
aaa	tgg	aca	gta	cas	cct	ata	gtg	ctg	cca	gaa	aaa	gat	agc	tgg	act	1056
Lys	Trp	Thr	Val	Xaa	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			

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ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val 35 40 45	144
gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu 115 120 125	384
aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly 130 135 140	432
aaa att aca aaa att ggg cct gaa aat ccg tac aat act cca ata ttt Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aar aac agt act aaa tgg aga aaa tta gta gac ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg 210 215 220	672
aar tat act gca ttt acc ata cct agt acg aat aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816

260										265					270					
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	gtg	gat	gat	ttg	ctt	gta	864				
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Leu	Val					
275										280					285					
gga	tct	gac	tta	gaa	ata	gag	cag	cat	aga	aca	aaa	ata	gag	gag	cta	912				
Gly	Ser	Asp	Leu	Glu	Ile	Glu	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu					
290										295					300					
aga	caa	cat	ctg	tgg	aag	tgg	gga	ttt	tac	aca	cca	gac	aaa	aaa	cat	960				
Arg	Gln	His	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His					
305										310					315					
cag	aaa	gaa	ccc	cca	ttc	ctt	tgg	atg	ggt	tat	gaa	ctc	cat	cct	gat	1008				
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp					
325										330					335					
aaa	tgg	aca	gka	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056				
Lys	Trp	Thr	Xaa	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr					
340										345					350					
gtc	aat	gac	ata	caa	aag	tta	gtg	gga	aaa	tta	aat	tgg	gca	agt	cag	1104				
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln					
355										360					365					
att	tat	cca	ggg													1116				
Ile	Tyr	Pro	Gly																	
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Ile	Val	Thr	Ile	Lys	Ile	Gly					
1				5				10				15								
ggg	caa	cta	aag	gaa	gct	cta	ata	gat	aca	gga	gca	gat	gat	aca	gta	96				
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Ile	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val					
20										25					30					
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	ata	ata	ggg	144				
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Ile	Ile	Gly					
35										40					45					
gga	att	gga	ggt	ctt	gtc	aaa	gta	aga	cag	tat	gat	cag	ata	ccc	ata	192				
Gly	Ile	Gly	Gly	Leu	Val	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile					
50										55					60					
gaa	atc	tgt	gga	cat	aaa	gtt	ata	ggt	aca	gtw	tta	gta	gga	cct	aca	240				
Glu	Ile	Cys	Gly	His	Lys	Val	Ile	Gly	Thr	Xaa	Leu	Val	Gly	Pro	Thr					
65										70					75					
cct	gcc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	ctt	ggt	tgc	act	288				

Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr		
				85					90					95			
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336	
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	ggg	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384	
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gag	aag	gag	gga	432	
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly		
	130					135					140						
aag	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480	
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
	145				150					155					160		
gcc	ata	aag	aaa	aag	aac	agt	act	agg	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asn	Ser	Thr	Arg	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165				170						175			
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576	
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
			180					185					190				
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aac	aaa	tca	gca	aca	gta	ctg	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Ala	Thr	Val	Leu		
		195				200						205					
gat	gtg	ggc	gat	gca	tat	ttt	tca	gtt	ccc	tta	gac	aaa	gaa	ttc	agg	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg		
	210				215						220						
aag	tat	act	gca	ttt	acy	ata	cct	agt	ata	aac	aat	gaa	aca	cca	ggg	720	
Lys	Tyr	Thr	Ala	Phe	Xaa	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
	225				230					235					240		
tar	ata	tca	gtg	tac	aat	gtr	ctt	cca	caa	gga	tgg	aaa	gga	tca	cma	768	
Xaa	Ile	Ser	Val	Tyr	Asn	Xaa	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Xaa		
			245						250					255			
gca	ata	ttc	maa	agt	agc	atg	aca	aga	atc	tta	gag	cct	ttt	aga	aaa	816	
Ala	Ile	Phe	Xaa	Ser	Ser	Met	Thr	Arg	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
			260					265					270				
caa	aat	cca	gaa	ata	gtt	atc	tat	caa	tac	gtg	gat	gat	ttg	tat	gta	864	
Gln	Asn	Pro	Glu	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val		
		275				280					285						
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	gta	gag	gaa	ctg	912	
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Val	Glu	Glu	Leu		
	290					295					300						
aga	caa	cat	ctg	ttg	agg	tgg	gga	ttt	ttc	aca	cca	gac	caa	aaa	cat	960	
Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Phe	Phe	Thr	Pro	Asp	Gln	Lys	His		
	305				310					315					320		
cag	aaa	gaa	ccc	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008	
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
				325					330					335			
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056	
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr		
			340					345					350				

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac gcn ggg 1116
Ile Tyr Ala Gly
370

<210> 30
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 30
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
1 5 10 15

ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30

tta gaa gaa atg agc tta cca gga aga tgg aaa cca aaa atg ata ggg 144
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

gga att gga ggk ttt atc aaa gtg agm cag tat gat cag ata ctc ata 192
Gly Ile Gly Xaa Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Leu Ile
50 55 60

gaa aty tgt gga cat aaa gct ata ggt aca gtr tta ata gga cct aca 240
Glu Xaa Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr
65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aaa 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110

cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggr 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Xaa
130 135 140

aaa att aca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
Lys Ile Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160

gcc ata aag aag aaa aac agt gat aaa tgg aga aaa tta gta gat ttc 528
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165 170 175

[illegible]

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<210> 31
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<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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<400> 31
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg      48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
  1                    5                    10                    15

ggg caa tta aag gaa gct cta tta gat aca gga gca gat gat aca gta      96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
                20                    25                    30

cta gaa gac gtg cat ttg cca gga aaa tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Val His Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
                35                    40                    45

gga att gga ggt ttt atc aaa gta aga cag tat gat gag gta ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Glu Val Pro Ile
  50                    55                    60

gaa ctc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Leu Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
  65                    70                    75                    80

ccc gtc aac ata att gga aga aat ctg wtg act caa ctt ggg tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Xaa Thr Gln Leu Gly Cys Thr
                85                    90                    95

cta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
                100                    105                    110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
                115                    120                    125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg      432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
  130                    135                    140

aaa att tca aga gtt ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Arg Val Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
  145                    150                    155                    160

gyc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc      528
Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
                165                    170                    175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
                180                    185                    190

ata cca cay ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa
                195                    200                    205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg
  210                    215                    220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly
  225                    230                    235                    240

att aga tac cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
                245                    250                    255

gca ata ttc caa agt agc atg aca aaa atc tta gat cct ttt agg aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys

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		260			265			270									
caa	aac	cca	gac	ata	gtt	atc	tat	caa	tac	gtg	gat	gat	ttg	tat	gta		864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val		
		275					280					285					
gga	tcy	gac	tta	gaa	ata	gga	cag	cat	agr	rca	aaa	ata	gaa	gaa	ctg		912
Gly	Xaa	Asp	Leu	Glu	Ile	Gly	Gln	His	Xaa	Xaa	Lys	Ile	Glu	Glu	Leu		
	290					295					300						
aga	caa	cat	ctg	ttg	aag	tgg	gga	ttt	acc	aca	cca	gac	aag	aaa	cat		960
Arg	Gln	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His		
305					310					315					320		
car	aaa	gaa	cct	cca	ttt	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat		1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
				325					330					335			
aaa	tgg	aca	gtg	cag	cct	ata	gtg	ctg	cca	gaa	aag	gac	agc	tgg	act		1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr		
			340				345						350				
gtc	aat	gac	ant	aca	gaa	gtt	agt	ggg	aaa	att	gaa	ttg	ggc	aag	tca		1104
Val	Asn	Asp	Xaa	Thr	Glu	Val	Ser	Gly	Lys	Ile	Glu	Leu	Gly	Lys	Ser		
		355					360					365					
gat	tta	tgc	agg	g													1117
Asp	Leu	Cys	Arg														
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<223>	Portion of HIV Reverse Transcriptase																
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Xaa	Val	Ala	Ile	Arg	Ile	Gly		
1				5					10					15			
ggg	caa	cta	aag	gaa	gcc	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta		96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val		
			20					25									

Pro	Val	Asn	Ile	Ile 85	Gly	Arg	Asn	Leu	Leu 90	Thr	Gln	Ile	Gly	Cys 95	Thr	
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gag Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	atc Ile	tgt Cys	aca Thr	gaa Glu	ttg Leu 140	gaa Glu	aag Lys	gaa Glu	gga Gly	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gct Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aaa Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttt Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	ggg Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tcc Ser	gtg Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttt Phe	aga Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	aya Xaa	cct Pro	sgt Xaa	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tcc Ser 255	cca Pro	768
gca Ala	ata Ile	ttt Phe	caa Gln 260	agc Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	wta Xaa	gtt Val	wtc Xaa	tat Tyr 280	caa Gln	twc Xaa	ata Ile	gat Asp	gat Asp 285	ctg Leu	tat Tyr	gta Val	864
ggc Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	cag Gln	cat His	ctg Leu	tgg Trp	aag Lys 310	tgg Trp	ggg Gly	ttt Phe	tac Tyr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttt Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	atg Met	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser	tgg Trp	act Thr	1056

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gtc aat gac ata cag aar tta gtg gga aaa ttg aat tgg gca agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg      1116
Ile Tyr Pro Gly
      370

<210> 33
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase

<400> 33
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
      1                      5                      10                      15

ggg caa cta aag gaa gct cta tta kat aca gga gca gat gat aca gtm      96
Gly Gln Leu Lys Glu Ala Leu Leu Xaa Thr Gly Ala Asp Asp Thr Xaa
      20                      25                      30

tta gaa gac atg act ttg cca gga aga tgg aaa cca aaa atg ata ggg      144
Leu Glu Asp Met Thr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
      35                      40                      45

gga att gga ggt ttt atc aaa gta aaa cag tat gag gag ata ccc ata      192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Glu Ile Pro Ile
      50                      55                      60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca      240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
      65                      70                      75                      80

cct gtc aac ata att gga aga aat ttg ttg act cag att ggt tgc act      288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
      85                      90                      95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aaa      336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
      100                      105                      110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa      384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
      115                      120                      125

aaa ata aaa gca ttw gta gaa att tgt gca gaa ctg gaa aag gaa ggg      432
Lys Ile Lys Ala Xaa Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly
      130                      135                      140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt      480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
      145                      150                      155                      160

gcc ata aag aaa aaa gac ggt act aaa tgg aga aag gta aca gat ttt      528
Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Val Thr Asp Phe
      165                      170                      175

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BOOK REVIEW

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<210> 34
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
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<220>
<221> CDS
<222> (0) ... (297)
<223> HIV Protease
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<221> CDS
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<223> Portion of HIV Reverse Transcriptase
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta ttr gac aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Xaa Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly	
35 40 45	
gga att gga ggt ttt att aaa gta aaa cag tat gaa cag ata acc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Ile Thr Ile	
50 55 60	
gam atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca	240
Xaa Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac gta att gga aga aat atg atg act cag att ggt tgc act	288
Pro Val Asn Val Ile Gly Arg Asn Met Met Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aac aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta cca aag aac aaa tca gta acg gta ctg	624
Ile Pro His Pro Ala Gly Leu Pro Lys Asn Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg	
210 215 220	
aag tac act gca ttt acc ata cct agg tat aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Arg Tyr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
act aga tat cag tac aat gtg ctt cct atg gga tgg aaa gga tca cca	768
Thr Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aga	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Arg	

260	265	270	
caa aat cca gac ata gtt atc tat Gln Asn Pro Asp Ile Val Ile Tyr	caa tac gtg gat gac ttg tat gta Gln Tyr Val Asp Asp Leu Tyr Val		864
275	280	285	
gga tct gac tta gag ata ggg cag cat aga gcg aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu			912
290	295	300	
aga gaa cat ctg tgg aag tgg ggt ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His			960
305	310	315	320
cag aaa gaa cct cca ttc cat tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe His Trp Met Gly Tyr Glu Leu His Pro Asp			1008
325	330	335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			1056
340	345	350	
gtc aat gac ata cag aaa tta gtg ggr aaa att gaa ttt ggg cga gtc Val Asn Asp Ile Gln Lys Leu Val Xaa Lys Ile Glu Phe Gly Arg Val			1104
355	360	365	
aga ttt amc caa ggg Arg Phe Xaa Gln Gly			1119
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1	5	10	15
ggg caa tta aag gaa gct cta cta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			96
20	25	30	
tta gaa gac atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly			144
35	40	45	
gga att gga ggt ttt atc aar gta aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile			192
50	55	60	
gaa atc tgt ggg cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr			240
65	70	75	80
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act			288

Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr	
				85					90					95		
cta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	gga	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
					150					155					160	
gcc	ata	aag	aaa	aag	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttt	tgg	gaa	gtc	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	tta	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	gga	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aag	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aag	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtc	ata	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
ggg	tct	gac	tta	gaa	ata	gga	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	caa	cac	ttg	ttg	maa	tgg	gga	ttc	acc	aca	cca	gac	aaa	aag	cat	960
Arg	Gln	His	Leu	Leu	Xaa	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
	305				310					315					320	
cag	aaa	gaa	ccc	cca	ttc	ctt	tgg	atg	ggt	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
			325						330					335		
aaa	tgg	aca	gta	cag	cct	ata	kaa	ctg	cca	gaa	aaa	gac	agc	tgg	ctg	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Xaa	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Leu	
			340					345					350			

tca atg aca tac aga aat tag tgg gaa agt tga att ggg caa gtc aaa	1104
Ser Met Thr Tyr Arg Asn * Trp Glu Ser * Ile Gly Gln Val Lys	
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ttt atg cng gg	1115
Phe Met Xaa	

<210> 36
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 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

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 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
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 <223> Portion of HIV Reverse Transcriptase

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1 5 10 15	

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	

gga att gga ggt ttt rtc aaa gta aga cag tat gat caa ata ccc ata	192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	

gaa atc tgt gga cat aaa gct aca ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Thr Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	

cct gyc aac ata att gga aga aat ctg ttg act cag att ggg tgc act	288
Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	

tta aat ttt cct att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ctg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	

aaa ata aaa gca tta gta gaa att tgt gca gaa ttg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Leu Glu Lys Glu Gly	
130 135 140	

aag att tca aaa att ggg ccy gaa aat cca tac aay act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Xaa Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	

gcc ata aag aaa aar aac agt act ara tgg aga aaa kta gta gat ttc	528
Ala Ile Lys Lys Lys Asn Ser Thr Xaa Trp Arg Lys Xaa Val Asp Phe	
165 170 175	

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aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga      576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
      180                      185                      190

ata cca cat ccc gca ggg cta aag aag aaa aaa tca gta aca gta ctg      624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu
      195                      200                      205

gat gtg ggt gat gca tat ttt tca gtt ccc ttg gat gaa gac ttc aga      672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
      210                      215                      220

aag tat aca gcc ttt acc tat act ggt tcc aac aat gag aca cca ggg      720
Lys Tyr Thr Ala Phe Thr Tyr Thr Gly Ser Asn Asn Glu Thr Pro Gly
      225                      230                      235                      240

att aga tat car tac aat gtg ctt cca cag gga tgg aaa gga tca cca      768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
      245                      250                      255

gca ata ttc caa agc agc atg aca aaa gtc tta gaa cct ttt aga aaa      816
Ala Ile Phe Gln Ser Ser Met Thr Lys Val Leu Glu Pro Phe Arg Lys
      260                      265                      270

caa aat cca gac ata gtt atc tgt caa tac atg gat gat ttg tat gta      864
Gln Asn Pro Asp Ile Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val
      275                      280                      285

gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg      912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu
      290                      295                      300

aga caa cat ctg tta agg tgg gga ttt tac aca cca gac gaa aaa cat      960
Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Glu Lys His
      305                      310                      315                      320

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gac      1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp
      325                      330                      335

aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act      1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr
      340                      345                      350

gtt aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gcc agt cag      1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
      355                      360                      365

att tac cca ggg
Ile Tyr Pro Gly
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<210> 37
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<212> DNA
<213> Human Immunodeficiency Virus (HIV)

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<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

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<221> CDS
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<223> Portion of HIV Reverse Transcriptase

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1				5					10					15			
ggg	caa	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96	
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val		
			20					25					30				
tta	gaa	gac	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg	144	
Leu	Glu	Asp	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly		
		35					40					45					
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	cag	gta	ccc	ata	192	
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Val	Pro	Ile		
	50					55					60						
gaa	atc	tgt	gga	cat	aaa	gct	ata	ggt	aca	gta	tta	gta	gga	cct	aca	240	
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr		
	65				70					75					80		
cct	gtc	aac	ata	att	gga	aga	aat	ctg	atg	aca	cag	ctt	ggt	tgt	act	288	
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Met	Thr	Gln	Leu	Gly	Cys	Thr		
				85					90					95			
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336	
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	gga	atg	gat	ggc	cca	aaa	ggt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384	
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	ggg	432	
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly		
	130					135					140						
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480	
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
	145				150					155					160		
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165					170					175			
agg	gaa	ctt	aat	aag	aaa	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	ggg	576	
Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
			180					185					190				
ata	cca	cat	cct	gca	gga	tta	aaa	aag	aat	aaa	tca	gta	aca	gta	ctg	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu		
		195					200					205					
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg		
	210				215						220						
aag	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720	
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
	225				230					235					240		
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768	
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro		
			245						250					255			
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	att	tta	gat	cct	ttt	aga	aaa	816	
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Asp	Pro	Phe	Arg	Lys		

	260	265	270	
cag aat cca gat ata gtt atc tat caa tac atg gat gat ttg tat gta				864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val				
	275	280	285	
gga tct gac tta gag ata ggg cag cat aga gca aaa ata gag gaa ctg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu				
	290	295	300	
aga gca cat ctg ttg aag tgg gga ttt acc acc cca gac aaa aaa cat				960
Arg Ala His Leu Leu Lys Trp Gly Phe Thr Pro Asp Lys Lys His				
	305	310	315	320
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp				
	325	330	335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act				1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr				
	340	345	350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag				1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
	355	360	365	
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Ile Tyr Ala Gly				
	370			
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cct caa tca ctt ctt tgg caa cga ccc mtc gtc aca ata aag gta ggg				48
Pro Gln Ser Leu Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Val Gly				
	1	5	10	15
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca ata				96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile				
	20	25	30	
tta gaa gac aya rat ttg cca ggg aga tgg aaa cca aaa ata ata ggg				144
Leu Glu Asp Xaa Xaa Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly				
	35	40	45	
gga att gga ggt ttt atc aga gta aga cag tat gat cag gta ccc ata				192
Gly Ile Gly Gly Phe Ile Arg Val Arg Gln Tyr Asp Gln Val Pro Ile				
	50	55	60	
gaa atc tgt gga cat aaa gtt gta agt aca gta tta gta gga cct aca				240
Glu Ile Cys Gly His Lys Val Val Ser Thr Val Leu Val Gly Pro Thr				
	65	70	75	80
cct gcc aac ata att gga aga aat ctg atg act cag att ggt tgc act				288

Pro	Ala	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Met	Thr	Gln	Ile	Gly	Cys	Thr		
				85					90					95			
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336	
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384	
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
			115				120					125					
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	gaa	gaa	ttg	gaa	aag	gat	ggg	432	
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Glu	Glu	Leu	Glu	Lys	Asp	Gly		
			130			135					140						
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480	
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
					150					155					160		
gcc	ata	aag	aaa	aag	aac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asn	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165					170					175			
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga	576	
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
				180				185					190				
ata	cca	cat	cct	gca	gga	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu		
				195			200					205					
gat	gtg	ggg	gat	gca	tat	ttt	tca	att	ccc	tta	gat	gaa	gac	ttc	aga	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Ile	Pro	Leu	Asp	Glu	Asp	Phe	Arg		
				210		215					220						
aag	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720	
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
					230					235					240		
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768	
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro		
				245					250					255			
tca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816	
Ser	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
				260				265					270				
caa	aat	cca	gac	ata	gtc	atc	tat	caa	tat	atg	gat	gat	ttg	tat	gta	864	
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
				275			280					285					
gga	tct	gac	tta	gag	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912	
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu		
				290		295					300						
aga	cag	cat	ctg	tgg	aag	tgg	ggg	ttt	tac	aca	cca	gac	ara	aaa	cat	960	
Arg	Gln	His	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Xaa	Lys	His		
					310					315					320		
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gac	1008	
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
				325					330					335			
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aag	gac	agc	tgg	act	1056	
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr		
				340				345					350				

aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtc caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca ggg tta aaa aag aac aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat raa gat tca gra	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Xaa Asp Ser Xaa	
210 215 220	
agt aca ctg cat tta cca tac cta gta cgr acc aat gag aca cca ggg	720
Ser Thr Leu His Leu Pro Tyr Leu Val Xaa Thr Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat caa tac aat gtg ctt cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac tta gtt atc tgt caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Leu Val Ile Cys Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gat tta gaa ata gag cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg tgg aag tgg ggg ttt tac aca cca gac aaa aaa cat	960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttc cgt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Arg Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta caa gcc tat aaa gct gcc aga aaa aga cag ctg gac	1056
Lys Trp Thr Val Gln Ala Tyr Lys Ala Ala Arg Lys Arg Gln Leu Asp	
340 345 350	
tgt caa tga cat tac mag aaa gtt agt ggg gaa aat tgg aat ttg ggg	1104
Cys Gln * His Tyr Xaa Lys Val Ser Gly Glu Asn Trp Asn Leu Gly	
355 360 365	
caa ggt cag att tat tgc cag ggg	1128
Gln Gly Gln Ile Tyr Cys Gln Gly	
370 375	

<210> 40
 <211> 1120
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1120)
 <223> Portion of HIV Reverse Transcriptase

<400> 40	
cct cag atc act ctt tgg caa cga ccc ctc gtt gca ata aag ata ggg Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Ala Ile Lys Ile Gly 1 5 10 15	48
gga cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	96
tta gaa gaa atg agt ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ccm rta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Xaa 50 55 60	192
gaa att tgc gga cat aaa gct gta ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt cct tta gat gaa gac ttc agr Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Xaa 210 215 220	672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tcc aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Ser Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc cta gaa cct ttt agg aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816

	260	265	270			
caa aat cca gat ata gtt atc tat caa tac atg gat gat cta tat gta	Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	275	280	285	864	
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg	Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	290	295	300	912	
aga caa cat ctg ttg agg tgg ggg ttt acc acc cca gac aaa aaa cat	Arg Gln His Leu Leu Arg Trp Gly Phe Thr Pro Asp Lys Lys His	305	310	315	960	
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	325	330	335	1008	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	340	345	350	1056	
gtc aat gac nat aca aaa gtt agt ggg gaa aat tga att ggg sca agt	Val Asn Asp Xaa Thr Lys Val Ser Gly Glu Asn * Ile Gly Xaa Ser	355	360	365	1104	
cag att tat tgg agg g	Gln Ile Tyr Trp Arg	370			1120	
<210> 41						
<211> 1059						
<212> DNA						
<213> Human Immunodeficiency Virus (HIV)						
<220>						
<221> CDS						
<222> (0)...(297)						
<223> HIV Protease						
<221> CDS						
<222> (298)...(1059)						
<223> Portion of HIV Reverse Transcriptase						
<400> 41						
cct caa atc act ctt tgg cag cga ccc gtt gtc aca ata aac ata ggg	Pro Gln Ile Thr Leu Trp Gln Arg Pro Val Thr Ile Asn Ile Gly	1	5	10	15	48
ggg caa cta aag gaa gct cta tta gac aca gga gca gat gat aca gta	Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val	20	25	30		96
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	35	40	45		144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata	Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	50	55	60		192
gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca	Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr	65	70	75	80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act						288

Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85					90					95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	ata	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aac	ccg	tac	aat	act	cca	gtc	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
					150					155					160	
gcc	ata	aag	aaa	aaa	gat	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aac	aag	aaa	act	caa	gac	ttc	tgg	gaa	att	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Ile	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195					200					205				
gat	gtg	ggg	gat	gca	tat	ttc	tca	gtt	cct	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aag	tat	act	gca	ttt	acc	ata	cct	agt	aca	aac	aat	gag	acg	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gcc	ata	nnn	nnn	nnn	nnn	nnn	nnn	nnn	nnn	nnn	nnn	nnn	nnn	nnn	nnn	816
Ala	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			260					265					270			
nnn	nnn	nnn	nnn	nnn	nnn	nnn	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	gag	cag	cat	aga	aca	aaa	ata	gag	aaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Glu	Gln	His	Arg	Thr	Lys	Ile	Glu	Lys	Leu	
	290					295					300					
aga	caa	cat	ctg	ttg	agg	tgg	gga	ttt	acc	aca	cca	gat	aaa	aaa	cat	960
Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
	305				310					315					320	
cag	aaa	gaa	cct	cca	ttt	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
			325						330					335		
aaa	tgg	aca	gta	cag	cct	ata	gta	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			

gtc
Val

1059

<210> 42
<211> 1053
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1053)
<223> Portion of HIV Reverse Transcriptase

<400> 42
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata arg ata ggg 48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Xaa Ile Gly
1 5 10 15
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
20 25 30
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45
gga att gga ggt ttt atm aaa gta aga cag tat gat cag ata cyc ata 192
Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile
50 55 60
gaa atc tgt gga yat aaa gct ata ggt acr gta tta gta gga ccc acg 240
Glu Ile Cys Gly Xaa Lys Ala Ile Gly Xaa Val Leu Val Gly Pro Thr
65 70 75 80
cct gtc aac rta att gga aga aat ctg wtg act cag att ggt tgc act 288
Pro Val Asn Xaa Ile Gly Arg Asn Leu Xaa Thr Gln Ile Gly Cys Thr
85 90 95
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa ttr gta gat ttc 528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Xaa Val Asp Phe
165 170 175
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtc caa tta gga 576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca kgg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Xaa	
225 230 235 240	
att aga tay cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata tty caa tgt agc atg aca aaa atc tta gag cct ttt aga aag	816
Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac cta gtt att tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg ara tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Xaa Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg gca gtg caa cct ata gtg ctg cca gaa aaa gac agc tgg	1053
Lys Trp Ala Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp	
340 345 350	
<210> 43	
<211> 1082	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1082)	
<223> Portion of HIV Reverse Transcriptase	
<400> 43	
cct caa atc act ctt tgg caa cga ccc ctt gtc aca rta aag rta ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Xaa Lys Xaa Gly	
1 5 10 15	
ggg caa cta aag gaa gct yta ttr gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Xaa Xaa Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat tta cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	

35					40					45						
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	cag	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile	
	50					55					60					
gaa	aty	tgt	ggg	cat	aaa	gct	ata	ggt	aca	gta	tta	gta	ggg	cct	aca	240
Glu	Xaa	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70					75					80	
cct	gtc	aac	ata	att	gga	aga	aat	ttg	ttg	act	cag	att	ggt	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85				90						95		
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	ccc	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	gta	gaa	att	tgt	aca	gaa	atg	gaa	aaa	gaa	ggg	432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aag	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttt	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	ccg	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aag	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu		
		195				200					205					
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
	210					215					220					
aaa	tat	ast	gca	ttt	acc	ata	ccg	agt	ata	aac	aat	gag	aca	cca	ggg	720
Lys	Tyr	Xaa	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	ccg	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	tgt	agc	atg	aca	aaa	atc	tta	gaa	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	ttg	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	cag	cat	ctg	ttg	aaa	tgg	ggr	ttt	acc	aca	cca	gac	aag	aaa	cat	960

[illegible]

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<210> 45
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
<220>
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<221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 45

cct cag atc act ctt tgg caa cga ccc rtc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gac gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat tta cca gga aaa tgg aaa cca aaa atg ata gtg	144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Val	
35 40 45	
gga att gga gga ttt gtc aaa gta aaa cag tat gag caa ata cct gta	192
Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Glu Gln Ile Pro Val	
50 55 60	
gaa atc tgt gga cat aaa gct gta ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gar	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu	
115 120 125	
aaa ata maa gca ttg gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Xaa Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gct ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asn Ser Asp Arg Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag agg act caa gac ttc tgg gaa att caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aag aaa tca gta aca rta cta	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Xaa Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca rtt ccc tta gat aaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Xaa Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	

Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Ser	Ile		
	50					55					60						
gaa	atc	tgt	gga	cat	aaa	gct	ata	ggg	aca	gta	tta	gta	gga	cct	aca	240	
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	80	
	65				70				75								
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	att	ggg	tgc	act	288	
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	95	
				85				90									
tta	aat	ttt	cct	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336	
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	110	
			100					105									
cca	gga	atg	gac	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384	
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	125	
		115					120										
aaa	ata	aaa	gca	tta	gta	gag	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga	432	
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	140	
	130					135											
aaa	att	tca	aaa	att	ggg	cct	gaa	aac	cca	tac	aat	act	cca	gta	ttt	480	
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	160	
	145				150					155							
gcc	ata	aag	aaa	aaa	gac	agt	act	aag	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	175	
				165					170								
aga	gaa	ctt	aat	aaa	aga	act	caa	gac	ttc	tgg	gag	gtt	caa	tta	gga	576	
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	190	
			180					185									
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	cta	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	205	
		195					200										
gat	gtg	ggc	gat	gca	tat	ttc	tca	gtt	ccc	tta	gat	gaa	gac	ttc	aga	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Asp	Phe	Arg	220	
	210					215											
aaa	tat	act	gca	ttt	acc	ata	cct	agt	ata	aac	aat	gag	aca	cca	ggg	720	
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	240	
	225				230					235							
act	aga	tat	cag	tac	aat	gtg	ctc	cca	cag	gga	tgg	aaa	gga	tca	cca	768	
Thr	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	255	
				245					250								
gca	ata	ttc	caa	tgt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816	
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	270	
			260					265									
caa	aat	cca	gac	cta	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864	
Gln	Asn	Pro	Asp	Leu	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	285	
		275					280										
gga	tct	gac	tta	gaa	ata	gga	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912	
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	300	
	290					295											
aga	caa	cat	ctg	ttg	agg	tgg	gga	ttt	acc	acc	cca	gac	aaa	aaa	cat	960	
Arg	Gln	His	Leu	Leu	Arg	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	315	
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[illegible]

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<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1115)
 <223> Portion of HIV Reverse Transcriptase

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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Ile Gly
 1 5 10 15

ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

ata gaa gac ata gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
 Ile Glu Asp Ile Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aaa cag tat gag cag gta ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Glu Gln Val Pro Ile
 50 55 60

gaa ctc tgt ggg cgt aaa act ata ggt aca gta tta gta gga cct aca 240
 Glu Leu Cys Gly Arg Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aac ctg atg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcy ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Xaa Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat cct gca ggg tta aaa aag aag aaa tca gta aca gta ttg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccg tta gat aaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
 210 215 220

aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg 720

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<220>
<221> CDS
<222> (0) ... (297)
<223> HIV Protease
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Xaa	Ile	Lys	Ile	Gly	
1				5					10					15		
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta																96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aag atg ata ggg																144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
		35					40					45				

gga att gga ggt ttc atc aaa gta aga cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgt ggc cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat cta ttg act cag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aag tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aaa act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cct gca ggg tta aaa aag aam aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg	
210 215 220	
aag tat acc gca ttt cca tcc cta gtt ata aac aat gag aca cca gga	720
Lys Tyr Thr Ala Phe Pro Ser Leu Val Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
atc aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa gta gag gag ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Val Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	

cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro 325 Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr 340 Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 350	
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agc cag	1104
Val Asn Asp 355 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 365	
att tac cca ggg	1116
Ile Tyr Pro Gly 370	
<210> 50	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0) ... (297)	
<223> HIV Protease	
<221> CDS	
<222> (298) ... (1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 50	
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Asn Ile Lys Ile Gly 1 5 10 15	
gga caa ctg aag gaa gct cta ttg gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ttg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly 35 40 45	
gga att gga ggt ttk gtc aaa gta aga cag tat gat cag ata cct gta	192
Gly Ile Gly Gly Xaa Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Val 50 55 60	
gaa att tgt gga cat aaa gyt ata ggt aca gtc tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Xaa Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag att ggc tgc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	
cca gga atg gat ggc ccg aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	

130	135	140	
aaa att tca aag att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160			480
gcc ata aag aaa aag aac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta mam aag aac aaa tca gta aca gtg cta Ile Pro His Pro Ala Gly Leu Xaa Lys Asn Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta tat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Tyr Glu Asp Phe Arg 210 215 220			672
aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tay aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc cag agt agc atg aca aga atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Arg Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gaa ata gtc atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gca tct gac tta gaa ata gag aaa cat aga aca aaa ata gag gaa ctg Ala Ser Asp Leu Glu Ile Glu Lys His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga caa cat ctg ttg agg tgg gga ttt tac aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aaa tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat gga ggg Ile Tyr Gly Gly 370			1116

<210> 51

<211> 1116

<212> DNA

<213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 51
 cct cag atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
 1 5 10 15
 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30
 tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45
 gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata cct ata 192
 Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60
 gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80
 cct gcc aac ata att gga aga gat ctg ttg act cag att ggt tgc act 288
 Pro Ala Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa ttg aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggt cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cct gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa aac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190
 ata cca cat ccc gcg ggg tta aaa aag aaa aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
 195 200 205
 gat gtg ggt gat gca tat ttt tca att ccc tta gat gaa gaa ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Glu Glu Phe Arg
 210 215 220
 aag tat act gca ttc acc ata cct agt ata aac aat gag aca cca ggg 720

000111" 50660450

Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
225					230					235					240	
gtt	aga	tat	caa	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Val	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	ccc	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tat	gtg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	gca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	caa	cat	ctg	tgg	agg	tgg	ggg	ttt	tac	aca	cca	gac	aaa	aaa	cat	960
Arg	Gln	His	Leu	Trp	Arg	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
	305				310					315					320	
cag	aaa	gaa	ccc	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
				325					330					335		
aaa	tgg	aca	gta	caa	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			
gtc	aat	gac	ata	cag	aaa	tta	gtg	ggg	aaa	ttg	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
		355					360					365				
att	tat	gca	ggg													1116
Ile	Tyr	Ala	Gly													
		370														
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<211>	1116															
<212>	DNA															
<213>	Human Immunodeficiency Virus (HIV)															
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<222>	(0)...(297)															
<223>	HIV Protease															
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<222>	(298)...(1116)															
<223>	Portion of HIV Reverse Transcriptase															
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cct	caa	atc	act	ctt	tgg	caa	cga	ccc	ctt	gtc	aca	ata	aag	rta	ggg	48
Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Thr	Ile	Lys	Xaa	Gly	
1				5					10					15		
ggg	caa	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atr	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Xaa	Ile	Gly	
		35					40					45				

gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ycc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Xaa Ile 50 55 60	192
gaa atc tgt gga cat aaa gct ata ggt tca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata aty gga aga aat ctg atg act cag att ggt tgc act Pro Val Asn Ile Xaa Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa ack gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Xaa Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gra gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Xaa Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gag atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aga att ggg ccc gaa aat cca tac aat act cca ata ttt Lys Ile Ser Arg Ile Ile Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe 145 150 155 160	480
gcc ata aag aaa aag aat agt act aga tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe 165 170 175	528
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aac aaa tca gtg aca gta ytg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Xaa 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt atr aac aat gag aaa cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Xaa Asn Asn Glu Lys Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca car gga tgg aaa ggg tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agc atg aca aaa aty tta gag cct ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Xaa Leu Glu Pro Phe Arg Lys 260 265 270	816
car aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ttg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg tta agg tgg gga ttt ttc aca cca gaa caa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Phe Thr Pro Glu Gln Lys His 305 310 315 320	960

130					135					140						
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aaa Lys	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
atc Ile	cca Pro	cat His 195	cct Pro	gca Ala	ggg Gly	tta Leu 200	aaa Lys	aag Lys	aaa Lys	aaa Lys	tca Ser 205	gta Val	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr 215	ttt Phe	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	cgg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe 230	acc Thr	ata Ile	cct Pro	agt Ser	aca Thr	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	gga Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln 245	tac Tyr	aat Asn	gtg Val	ctt Leu	cca Pro	caa Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe 260	caa Gln	agt Ser	agc Ser	atg Met	aca Thr 265	aaa Lys	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	agg Arg	aat Asn	816
aaa Lys	aat Asn 275	cca Pro	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	cta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	gca Ala 300	aaa Lys	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	gaa Glu	cat His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	ggg Gly	ttt Phe	act Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr 340	gtc Val	cag Gln	cct Pro	ata Ile	gag Glu 345	ctg Leu	cca Pro	gaa Glu	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn 355	gac Asp	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn 365	tgg Trp	gca Ala	agt Ser	cag Gln	1104
att Ile	tat Tyr 370	gca Ala	gga Gly													1116

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<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Xaa Val Thr Ile Lys Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct yta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata gtg 144
 Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val
 35 40 45

gga att gga ggt ttt gtc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60

gaa atc tgt gga cat aaa att ata ggt aca gta tta ata gga aat aca 240
 Glu Ile Cys Gly His Lys Ile Ile Gly Thr Val Leu Ile Gly Asn Thr
 65 70 75 80

cct gcc aac gta att gga aga aat ctg ttg act cag ctt ggt tgc act 288
 Pro Ala Asn Val Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gat ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aag gac agt act aaa tgg aga aaa gta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe
 165 170 175

aga gaa ctt aac aag aga act caa gac ttc tgg gag gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cac ccc gca ggg ata aaa aag aat aaa tca gta act gta cta 624
 Ile Pro His Pro Ala Gly Ile Lys Lys Asn Lys Ser Val Thr Val Leu
 195 200 205

gat gta ggt gat gca tat ttc tca gtt ccc tta gat gaa gac ttc aga 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg
 210 215 220

aaa tat act gca ttc acc ata cct agt att aac aat gag aca cca ggg 720

Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
225					230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctc	cca	cag	gga	tgg	aaa	gga	tca	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cac	aga	ata	aaa	ata	rag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Ile	Lys	Ile	Xaa	Glu	Leu	
	290					295					300					
aga	gaa	cat	cta	tgg	aag	tgg	gga	ttt	tac	aca	cca	gac	aaa	aag	cat	960
Arg	Glu	His	Leu	Trp	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
305				310				315							320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggt	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
			325					330						335		
aaa	tgg	aca	gta	cag	cct	ata	acg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056
Lys	Trp	Thr	Val	Gln	Pro	Ile	Thr	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340				345						350			
gtc	aat	gac	ata	cag	aag	tta	gtg	ggg	aaa	ttg	aat	tgg	gca	agt	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	
		355					360					365				
att	tat	gca	ggg													1116
Ile	Tyr	Ala	Gly													
		370														
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<213> Human Immunodeficiency Virus (HIV)																
<220>																
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<223> Portion of HIV Reverse Transcriptase																
<400> 55																
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Pro	Gln	Ile	Thr	Leu	Trp	Gln	Arg	Pro	Leu	Val	Ala	Ile	Lys	Ile	Gly	
1				5				10					15			
ggg	caa	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gat	gat	aca	gtc	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val	
			20					25					30			
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg	144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
			35				40					45				

gga att gga ggt ttt atc aaa gta aag cag tat gat cag gta ctt gta Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Val Leu Val	192
50 55 60	
gaa att tgt gga cat ara gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Xaa Ala Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgt act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	288
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	
cca ggt atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aaa ata aaa gca tta ata gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gcc ata aag aaa aaa gac agt acc aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
aga gaa ctt aat aag aaa acg caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Lys Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aag gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	672
210 215 220	
aag tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly	720
225 230 235 240	
att aga tat cag tac aat gtg ctg cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca ata ttt caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816
260 265 270	
caa aat cca gac atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	864
275 280 285	
gga tct gac tta gaa ata gag cag cat aga rca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Xaa Lys Ile Glu Glu Leu	912
290 295 300	
agg cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	960
305 310 315 320	

130				135				140								
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gat Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gta Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	ggg Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	cta Leu	624
gat Asp	gtg Val 210	ggg Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	672
aag Lys 225	tat Tyr	act Thr	gca Ala	ttc Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agc Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	att Ile	tta Leu	gaa Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gaa Glu	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	atg Met	gat Asp 285	gat Asp	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	raa Xaa	ata Ile	gag Glu 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aag Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggg Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gtg Val 345	ctg Leu	cca Pro	gaa Glu	cag Gln	gac Asp 350	agc Ser	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	tta Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
att Ile	tat Tyr 370	cca Pro	ggg Gly													1116

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<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 57
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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Val Lys Leu Gly
 1 5 10 15
 ggg caa cta atg gaa gtt cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Met Glu Val Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30
 rta gaa gaa ata agt tta cca gga aga tgg aaa cca aaa atg ata ggg 144
 Xaa Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ttt gtc aaa gta aaa cag tat gat cag gta ccc tta 192
 Gly Ile Gly Gly Phe Val Lys Val Lys Gln Tyr Asp Gln Val Pro Leu
 50 55 60
 gaa att tgt gga aaa aag gct ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly Lys Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80
 cct gcc aac ata att gga aga aat ttt ttg gct cag att ggt tgc act 288
 Pro Ala Asn Ile Ile Gly Arg Asn Phe Leu Ala Gln Ile Gly Cys Thr
 85 90 95
 tta aat ttc ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aag aac agt act aga tgg aga aaa tta gta gat ttt 528
 Ala Ile Lys Lys Lys Asn Ser Thr Arg Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aag agg acs caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Xaa Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190
 ata cca cat ccc gca ggg tta aar aag aac aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
 195 200 205
 gat gtg ggt gat gca tat ttt tca gtt ccc tta gat cca gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Pro Asp Phe Arg
 210 215 220
 aag tat act gca ttt acc ata cct agt aca aac aat gag aca cca ggg 720

Lys 225	Tyr	Thr	Ala	Phe	Thr 230	Ile	Pro	Ser	Thr	Asn 235	Glu	Thr	Pro	Gly 240		
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	caa Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cca Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	atg Met	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	ata Ile	gag Glu 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	tac Tyr 315	aca Thr	cca Pro	gac Asp	caa Gln	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggg Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr 340	gta Val	cag Gln	cct Pro	ata Ile	acg Thr	ctg Leu 345	cca Pro	gac Asp	aaa Lys	gac Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn 355	gac Asp	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	tta Leu	aat Asn 365	tgg Trp	gca Ala	agt Ser	cag Gln	1104
att Ile	tat Tyr 370	gca Ala	ggg Gly													1116
<210> 58																
<211> 1116																
<212> DNA																
<213> Human Immunodeficiency Virus (HIV)																
<220>																
<221> CDS																
<222> (0)...(297)																
<223> HIV Protease																
<221> CDS																
<222> (298)...(1116)																
<223> Portion of HIV Reverse Transcriptase																
<400> 58																
cct Pro 1	caa Gln	atc Ile	act Thr	ctt Leu 5	tgg Trp	caa Gln	cga Arg	ccc Pro	cta Leu 10	gtt Val	aca Thr	ata Ile	aaa Lys	ata Ile 15	ggg Gly	48
ggg Gly	caa Gln	cta Leu	aag Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp 30	gat Asp 30	aca Thr	gta Val	96
tta Leu	gaa Glu	gaa Glu 35	atg Met	act Thr	ttg Leu	cca Pro	gga Gly 40	aaa Lys	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	ggg Gly	144

gga att gga ggt ttt atc aaa gta aga car tat gat cag ata ctc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag atc ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aar caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat cca gca ggg tta aaa aag aaa aaa tca gta aca gta ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca ata atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Ile Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga cag cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	

cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata aag ctg cca gac aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Asp Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat gca gga	1116
Ile Tyr Ala Gly	
370	
<210> 59	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
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<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 59	
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Xaa	
1 5 10 15	
ggg caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa ata aat ttg cca ggg aaa tgg aaa cca maa atg ata ggg	144
Leu Glu Glu Ile Asn Leu Pro Gly Lys Trp Lys Pro Xaa Met Ile Gly	
35 40 45	
gga att gga ggt ttt att aaa gta aga cag tat gat caa ata gcc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Ala Ile	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta rta gaa atc tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Xaa Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	

130	135	140	
aaa att tca aaa att Lys Ile Ser Lys Ile 145	ggg cct gaa aat cca Gly Pro Glu Asn Pro 150	tac aat act cca gta ttt Tyr Asn Thr Pro Val Phe 155	480
gcm ata aag aaa Xaa Ile Lys Lys 165	gac agt act aaa tgg Asp Ser Thr Lys Trp 170	aga aaa tta gta gat ttc Arg Lys Leu Val Asp Phe 175	528
aga gaa ctt aat aag Arg Glu Leu Asn Lys 180	aga act caa gac ttc Arg Thr Gln Asp 185	tgg gaa gtc caa tta gga Trp Glu Val Gln Leu Gly 190	576
ata cca cat ccc gca Ile Pro His Pro Ala 195	ggg tta aaa aag aaa Gly Leu Lys Lys Lys 200	tca gta aca gta cta Ser Val Thr Val Leu 205	624
gat gtg ggt gat gca Asp Val Gly Asp Ala 210	tat ttc tca gtt ccc Tyr Phe Ser Val Pro 215	tta gac caa gac ttc Leu Asp Gln Asp Phe 220	672
aag tat act gca ttt Lys Tyr Thr Ala Phe 225	acc ata cct agt ata Thr Ile Pro Ser Ile 230	aac aat gag aca cca Asn Asn Glu Thr Pro 235	720
att aga tat cag tac Ile Arg Tyr Gln Tyr 245	aat gtg ctt cca cag Asn Val Leu Pro Gln 250	gga tgg aaa gga tca Gly Trp Lys Gly Ser 255	768
gca ata ttc caa agt Ala Ile Phe Gln Ser 260	agc atg aca agg atc Ser Met Thr Arg Ile 265	tta gar cct ttt aga Leu Glu Pro Phe Arg 270	816
caa aat cca gaa ata Gln Asn Pro Glu Ile 275	gtc aty tat cag tac Val Xaa Tyr Gln Tyr 280	atg gat gat tta tat Met Asp Asp Leu Tyr 285	864
gga tct gac tta gaa Gly Ser Asp Leu Glu 290	ata ggg cag cat aga Ile Gly Gln His Arg 295	aca aaa gta gag gaa Thr Lys Val Glu Glu 300	912
aga caa cat ctg ttg Arg Gln His Leu Leu 305	agr tgg ggg ttt tmc Xaa Trp Gly Phe Xaa 310	acg cca gac aaa aag Thr Pro Asp Lys Lys 315	960
cag aaa gaa cct cca Gln Lys Glu Pro Pro 325	ttc ctt tgg atg ggt Phe Leu Trp Met Gly 330	tat gaa ctc cat cct Tyr Glu Leu His Pro 335	1008
aaa tgg aca gta cag Lys Trp Thr Val Gln 340	act ata gaa ctg cca Thr Ile Glu Leu Pro 345	gat agc tgg act Ser Asp Ser Trp Thr 350	1056
gtc aat gac ata cag Val Asn Asp Ile Gln 355	aag tta gtg gga aaa Lys Leu Val Gly Lys 360	ttg aat tgg gca agt Leu Asn Trp Ala Ser 365	1104
ata tac cca ggg Ile Tyr Pro Gly 370			1116

<210> 60
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

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50 55 60	
gaa att tgt gga cat aag gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	240
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag mtt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Xaa Gly Cys Thr	288
85 90 95	
tta aat ttt ccc atc agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gag gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	432
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt Lys Ile Ser Lys Ile ggg cct gaa aat cca tac aat act cca ata ttt	480
145 150 155 160	
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt cag tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa agc ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Ser Phe Arg	672
210 215 220	
aag tac act gca ttt acc ata ccc agt aca aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	720
225 230 235 240	
rca aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816
260 265 270	
caa aat cca gaa atg gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Glu Met Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val	864
275 280 285	
gga tct gac tta gag ata gag caa cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	912
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	960
305 310 315 320	

[illegible]

-101-

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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gga cag cta acg gaa gct yta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Thr Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg act ttg cca gga aaa tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Thr Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly
 35 40 45

ggr att gga ggt ttt atc aaa gta aga cag tat gat cac gta ctt gta 192
 Xaa Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp His Val Leu Val
 50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat ttg atg act cag ctt ggg ttc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr
 85 90 95

tta aat ttt cca att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca ggg atg gat ggc cca aaa gtt aaa caa tgg cca ttg mca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Xaa Glu Glu
 115 120 125

aaa ata aaa gca cta aca gaa att tgt aca gaa ttg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140

aaa att tca aga ata ggg cct gaa aat cca tac aat act cca ata ttt 480
 Lys Ile Ser Arg Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
 145 150 155 160

gcc ata aag aag aaa aac ggt ayt agg tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asn Gly Xaa Arg Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gag cta aat aag aga act caa gac ttc tgg gaa gtt caa cta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat cct gca gga cta aaa aag aac aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta cat gaa gac ttt aga 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu His Glu Asp Phe Arg
 210 215 220

aag tat acc gca ttc acc ata cct agt aca aac aat gaa aca cca gga 720

[illegible]

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<210> 64
<211> 1116
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
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<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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Gly Ile Gly Xaa Phe Xaa Lys 55 Val Arg Gln Tyr Asp 60 Gln Ile Xaa Ile	
50	
gaa atc tgc gga cat aaa gct ata ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val 75 Leu Val Gly Pro Thr 80	
65	
cct gyc aac ata att gga aga aat ctg ttg act cag ctt ggg tgc act	288
Pro Xaa Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 95	
85	
tta aat ttt ccc att agt cct att gaa act gta cca gta caa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Gln Leu Lys 110	
100	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 125	
115	
aag ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 140	
130	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 160	
145	
gct ata aag aaa aag gac agt gct aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Ala Lys Trp Arg Lys Leu Val Asp Phe 175	
165	
agg gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 190	
180	
ata cck cat ccc gca ggg ttr aaa aag aaa aaa tca gta aca gta cta	624
Ile Xaa His Pro Ala Gly Xaa Lys Lys Lys Lys Ser Val Thr Val Leu 205	
195	
gat gta ggt gat gca tat ttt tca gtt ccc tta gat caa aac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Gln Asn Phe Arg 220	
210	
aag tat act gca ttc acc ata cct agt ata aac aat gag ayg cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly 240	
225	
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 255	
245	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 270	
260	
caa aat cca gar ata rtt atc tat caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Glu Ile Xaa Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 285	
275	
gga tct gac ttr gaa ata ggg cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Xaa Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 300	
290	
aga caa cat ytg ttg aag tgg gga ttt acc aca cca gac aag aag cat	960
Arg Gln His Xaa Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 320	
305	
310	
315	

130	135	140	
aaa att tca aaa att ggg cct gaa aay cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctr Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gaa ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220			672
aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
rtt aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Xaa Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa aat cca gac ata att atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Ile Ile Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285			864
gga tct gat ttg gaa ata gag cag cat aga aca aaa ata gag gaa cta Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga gaa cat ctg tgg aag tgg gga ttt tac aca cca gac aaa aaa cat Arg Glu His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata aag ytg cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Lys Xaa Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt caa Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tat cca ggg Ile Tyr Pro Gly 370			1116

<210> 66
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 66

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1 5 10 15	
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gak rca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Xaa Xaa Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta agr car tat gac cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgt gga cag aaa gct ata ggt aca gta tta gta gga cct acm	240
Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Val Gly Pro Xaa	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act caa att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gca gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Ala Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt aat ara tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Asn Xaa Trp Arg Lys Leu Val Asp Phe	
165 170 175	
agg gaa ctc aat aag aga act caa gac ttc tgg gaa gtt caa tta ggc	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca rta ctr	624
Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Xaa Xaa	
195 200 205	
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aar tat act gca ttt acc ata cct agt aca wac aat gag aca cca ggg	720

Lys 225	Tyr	Thr	Ala	Phe	Thr 230	Ile	Pro	Ser	Thr 235	Xaa	Asn	Glu	Thr	Pro	Gly 240	
att Ile	aga Arg	tat Tyr	cag Gln	krc Xaa 245	aat Asn	gtg Val	yyt Xaa	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tcm Xaa 255	cca Pro	768
gca Ala	ata Ile	ttc Phe 260	mam Xaa 260	agt Ser	agc Ser	ayg Xaa	aca Thr	aaa Lys 265	att Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
caa Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tgt Cys 280	caa Gln	tac Tyr	gtg Val	gat Asp	gat Asp 285	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser	gac Asp	tta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ttg Leu	912
agg Arg 305	caa Gln	cat His	ttg Leu	ttg Leu	agg Arg 310	tgg Trp	ggr Xaa	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	ara Xaa	aaa Lys	cat His 320	960
cag Gln	aaa Lys	gag Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr 340	gta Val	cag Gln	cct Pro	ata Ile	aaa Lys	ctg Leu 345	cca Pro	gaa Glu	aaa Lys	gay Asp	agc Ser 350	tgg Trp	act Thr	1056
gtc Val	aat Asn	gac Asp 355	ata Ile	cag Gln	aag Lys	tta Leu	gtg Val 360	gga Gly	aaa Lys	ttg Leu	aat Asn	tgg Trp 365	gca Ala	agt Ser	cag Gln	1104
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<210> 67																
<211> 1119																
<212> DNA																
<213> Human Immunodeficiency Virus (HIV)																
<220>																
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<222> (0)...(297)																
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<223> Portion of HIV Reverse Transcriptase																
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ggg Gly	caa Gln	cta Leu	aag Lys 20	gaa Glu	gct Ala	cta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gta Val	96
cta Leu	gaa Glu	gaa Met 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aga Arg	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	atg Met	ata Ile	ggg Gly	144

gga att gga ggt ttt aty aaa gta aga cag tat gat cag ata tcc ata Gly Ile Gly Gly Phe Xaa Lys Val Arg Gln Tyr Asp Gln Ile Ser Ile 50 55 60	192
gaa atc tgt ggg cat aaa gtt aca ggt aca gtg tta ata gga cct aca Glu Ile Cys Gly His Lys Val Thr Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca ttg gta gaa att tgt gca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Ala Glu Met Glu Lys Glu Gly 130 135 140	432
caa att tca aaa att gag cct gaa aat cca tac aat aat cca gta ttt Gln Ile Ser Lys Ile Glu Pro Glu Asn Pro Tyr Asn Asn Pro Val Phe 145 150 155 160	480
gtc ata aag aaa aaa gac ggt act aac tgg aga aaa tta ata gat ytc Val Ile Lys Lys Lys Asp Gly Thr Asn Trp Arg Lys Leu Ile Asp Xaa 165 170 175	528
aga gaa ctt aat aag aga act caa gat ttc tgg gaa att caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aat aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca ttt tat tca gtt ccc tta gat gag aac ttc agg Asp Val Gly Asp Ala Phe Tyr Ser Val Pro Leu Asp Glu Asn Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca atg gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Met Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
aac aat cca gac ata gtc atc tat caa tac atg gat gat ttg tat gta Asn Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gca tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga gaa cat cta ttr aag tgg gga ttt acc aca cca gac aar aar yat Arg Glu His Leu Xaa Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys Xaa 305 310 315 320	960

cag aaa gaa cct cca ytc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Xaa Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
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355 360 365	
att tat cca ggg att	1119
Ile Tyr Pro Gly Ile	
370	
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<222> (0)...(297)	
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<223> Portion of HIV Reverse Transcriptase	
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1 5 10 15	
gga caa cta aaa gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca ggg aaa tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga atc gga gga ttt atc aaa gta aga cag tat gag cag ata cac ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Ile His Ile	
50 55 60	
gaa atc tgt ggg cat aaa gct ata ggt aca gtr tta ata gga ccc aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Xaa Leu Ile Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act cag att ggc tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	

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<210> 69
<211> 1119
<212> DNA
<213> Human Immunodeficiency Virus (HIV)
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<220>
 <221> CDS
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<221> CDS
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ggg caa yta aag gaa gct mta tta gay aca gga gca gat gat aca gtg 96
 Gly Gln Xaa Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa ata ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga gag tat gag cag ata caa gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Glu Tyr Glu Gln Ile Gln Val
 50 55 60

gaa atc tgt gga cat aag gct ata rgt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Xaa Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga aga aat cta atg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gag act gta ccg gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat acy ccr gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Xaa Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata ccg cat ccc gca ggg tta aag aag aaa aaa tca gta aca gta ctr 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Xaa
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg
 210 215 220

aag tac act gca ttt acc ata cct agt ata aac aat gag aca cca gga 720

09709905-11000

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gaa Glu 65	atc Ile	tgt Cys	gga Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggt Gly	aca Thr	gta Val 75	tta Leu	ata Ile	gga Gly	cct Pro	aca Thr 80	240
cct Pro	gtc Val	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aay Asn	ctg Leu	ttg Leu 90	aca Thr	cag Gln	att Ile	ggt Gly	tgy Cys 95	act Thr	288
tta Leu	aat Asn	ttt Phe	ccc Pro 100	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val 110	aaa Lys	tta Leu	aag Lys	336
cca Pro	gga Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	ara Xaa 120	gty Xaa	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys 130	ata Ile	aar Lys	gca Ala	tta Leu	atg Met	gaa Glu 135	att Ile	tgt Cys	gca Ala	gay Asp	atg Met 140	gaa Glu	aag Lys	gaa Glu	ggr Xaa	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcy Xaa	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agc Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aaa Lys	act Thr	caa Gln	gac Asp 185	ttt Phe	tgg Trp	gaa Glu	gtc Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccy Xaa	gca Ala	ggg Gly	tta Leu 200	aaa Lys	aag Lys	aac Asn	aaa Lys	tca Ser 205	gta Val	aca Thr	gta Val	ttg Leu	624
gat Asp	gtg Val 210	ggt Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccy Xaa	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
aaa Lys 225	tay Tyr	act Thr	gca Ala	ttt Phe	acm Xaa 230	ata Ile	cct Pro	agt Ser	ata Ile	aat Asn 235	aat Asn	gca Ala	aca Thr	cca Pro	ggg Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
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cag Gln	aat Asn	cca Pro 275	gac Asp	ata Ile	gtt Val	atc Ile	tat Tyr 280	caa Gln	tac Tyr	atg Met	gat Asp 285	gay Asp	ttg Leu	tat Tyr	gta Val	864
gga Gly	tct Ser 290	gac Asp	tta Leu	gaa Glu	mta Xaa	ggg Gly 295	cag Gln	cat His	aga Arg	rca Xaa	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cat His	ctg Leu	tta Leu 310	agg Arg	tgg Trp	ggg Gly	ttt Phe	acc Thr 315	acw Xaa	cca Pro	gac Asp	aag Lys	aaa Lys 320	cat His	960

cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta car ccc ata gtg ttg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
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Ile Tyr Xaa Gly Ile	
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1 5 10 15	
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Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aag cca aaa atg ata gtg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Val	
35 40 45	
gga att gga ggt ttt agc aaa gta aga caa tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ser Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgc gga cgt aaa gtt gta ggt tca gta tta ata gga cct aca	240
Glu Ile Cys Gly Arg Lys Val Val Gly Ser Val Leu Ile Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggc tgt act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca aaa gag	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Lys Glu	
115 120 125	
aaa ata aaa gca tta ata gaa att tgt aca gaa ttg gaa gaa gma gga	432
Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Leu Glu Glu Xaa Gly	

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<213> Human Immunodeficiency Virus (HIV)

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<223> Portion of HIV Reverse Transcriptase
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gaa atc tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga gat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gat act gta cca gta aaa tta aaa Leu Asn Phe Pro Ile Ser Pro Ile Asp Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta gta gaa att tgt aca gaa ctg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Lys Glu Gly 130 135 140	432
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ata cca cat ccc gcg ggg tta aaa aag aac aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Asn Lys Ser Val Thr Val Leu 195 200 205	624
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Gln Lys Glu Pro Pro Phe Leu Trp Met Xaa Tyr Glu Leu His Pro Asp	
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Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr	
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Ile Tyr Pro Gly Ile	
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Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gag gaa cta aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Leu Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
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Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa ata tgt gga cat aaa gct att ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aac ttg ttg act cag ctt ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
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Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly	

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aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	tta Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	ggg Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gtc Val	ctg Leu	624
gat Asp	gtg Val 210	ggg Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gaa Glu	ttc Phe	agg Arg	672
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aga Arg 305	cag Gln	cat His	ctg Leu	ttg Leu	agg Arg 310	tgg Trp	gga Gly	ttt Phe	acc Thr	aca Thr 315	cca Pro	gac Asp	aaa Lys	aag Lys	cat His 320	960
cag Gln	aaa Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggt Gly 330	tat Tyr	gag Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
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-121-

SECRET

- 122 -

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Gly																	
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Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	Lys	Tyr	Thr		
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Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro		
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tta gaa gac atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45	144
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cct gtc aac ata att gga aga aat ctg ttg act caa ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr 85 90 95	288

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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
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Ala	Ile	Lys	Lys	Lys	Asn	Ser	Thr	Arg	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
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Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
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Arg	Gln	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
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Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agc	cag	1104
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	

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	tta gaa gac atg gat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly 35 40 45					144
	gga att gga ggt ttt atc aaa gta aaa cag tat gat cag ata ccc ata Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile 50 55 60					192
	gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80					240
	cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Thr Gln Leu Gly Cys Thr 85 90 95					288
	tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110					336
	cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125					384
	aaa ata aaa gca ttg gta gaa ata tgt aca gaa atg gaa aag gaa ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140					432
	aaa att tca aaa att ggg cct gaa aat cca tac aat acr cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Xaa Pro Val Phe 145 150 155 160					480
	gcc ata arg aaa aaa gaa agc tct agc tct aaa tgg aga aaa tta gta Ala Ile Xaa Lys Lys Glu Ser Ser Ser Ser Lys Trp Arg Lys Leu Val 165 170 175					528
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[illegible]

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<400> 79
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ggg	caa	cta	aag	gaa	gct	cta	tta	gat	aca	gga	gca	gac	aat	aca	gta	96
Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asn	Thr	Val	
			20					25					30			
ttc	gaa	gac	ctg	gat	tta	cca	gga	agg	tgg	aaa	cca	aaa	atg	ata	ggg	144
Phe	Glu	Asp	Leu	Asp	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly	
		35					40					45				
gga	att	gga	ggt	ttt	atc	aaa	gta	aaa	cag	tat	gag	cag	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Lys	Gln	Tyr	Glu	Gln	Ile	Pro	Ile	
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Glu	Ile	Cys	Gly	Arg	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
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cct	gtc	aac	ata	att	gga	aga	gat	ctg	ttg	act	cag	att	ggt	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asp	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
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cca	gga	atg	gat	ggc	cca	aga	gtt	aaa	caa	tgg	cca	ttg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Arg	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
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Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Ala	Glu	Met	Glu	Lys	Glu	Gly	
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aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt	480
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145					150					155					160	
gcc	ata	aag	aaa	aag	aac	agt	aat	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asn	Ser	Asn	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aag	tca	ata	aca	gta	tta	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Ile	Thr	Val	Leu	
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gat	gtg	ggt	gat	gca	tat	ttc	tca	gtt	ccc	tta	gat	gaa	gac	ttc	agg	672
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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
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Gly	Ser	Asp	Leu	Glu	Ile	Glu	Gln	His	Arg	Thr	Lys	Ile	Asp	Glu	Leu		
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aga	caa	cat	ctg	ttg	agg	tgg	gga	ctt	acc	aca	cca	gac	cag	aaa	cat		960
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
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Gly	Gln	Leu	Lys	Glu	Ala	Leu	Leu	Asp	Thr	Gly	Ala	Asp	Asp	Thr	Val		
			20					25					30				
tta	gaa	gaa	atg	aat	ttg	cca	gga	aga	tgg	aaa	cca	aaa	atg	ata	ggg		144
Leu	Glu	Glu	Met	Asn	Leu	Pro	Gly	Arg	Trp	Lys	Pro						

COPIES

																85																	90																	95																
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Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly																																																			
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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val																																																			
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gga	tct	gac	tta	gaa	ata	ggg	cag	cat	agg	aca	aaa	ata	gag	gaa	ctg																	912																																		
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<223> HIV Protease

<221> CDS
<222> (298)...(1116)
<223> Portion of HIV Reverse Transcriptase
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THEORY OF

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cag aaa gaa cct cca ttc ctk tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Xaa Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
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ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val 20 25 30			96
tta gaa gac atg agt tta cca gga aaa tgg aaa cca aaa atg ata ggg Leu Glu Asp Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly 35 40 45			144
gga att gga ggt ttt atc aaa gta aga cag tat gat caa gta ccc ata Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Pro Ile 50 55 60			192
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80			240
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act			288

Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr		
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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
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Ala	Tyr	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
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gga	tct	gac	tta	gag	ata	gga	cag	cat	aga	gca	aaa	ata	gag	gac	cta	912	
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	290					295					300						
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Arg	Ala	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His		
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
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<221> CDS
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 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

 tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
 35 40 45

 gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta agc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Ser Ile
 50 55 60

 gaa atc tgt gga cat aaa gct ata ggt aca gta tta ata gga ccc acc 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

 cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Thr Gln Leu Gly Cys Thr
 85 90 95

 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

 cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gag aag gaa ggr 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Lys Glu Xaa
 130 135 140

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 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

 gcc ata aar aaa aaa gac agt act aaa tgg aga aag tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

 aga gaa ctt aat aaa ara act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Xaa Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

 ata cca cat ccc gca ggg tta aaa aag aam aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Xaa Lys Ser Val Thr Val Leu
 195 200 205

 gay gtg ggt gat gcr tat ttt tca gtt ccy tta gay aaa gay ttc agg 672
 Asp Val Gly Asp Xaa Tyr Phe Ser Val Xaa Leu Asp Lys Asp Phe Arg
 210 215 220

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 Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Xaa Pro Gly
 225 230 235 240

 att aga tat cag tac aat gtg ctt cca car gga tgg aaa gga tca cca 768
 Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro
 245 250 255

 gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aar 816
 Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys

0970606-11000

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maa aat cca gac ata gty atc tay caa tac atg gat gat ttr tat gta				864
Xaa Asn Pro Asp Ile Xaa Ile Tyr Gln Tyr Met Asp Asp Xaa Tyr Val	275	280	285	
gga tct gac tta gaa ata gga cag cat aga aca aaa ata gag gaa ctg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	290	295	300	
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Arg Gln His Leu Leu Gln Trp Gly Leu Thr Thr Pro Asp Lys Lys His	305	310	315	320
cag aaa gaa cct cca ttc ctt tgg atg ggg tat gaa ctc cat ccg gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	325		330	335
aaa tgg aca gta cag cct ata wtg ctg cca gac aaa gac agc tgg act				1056
Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Asp Lys Asp Ser Trp Thr	340		345	350
gtm aat gac ata cag aar tta gta gga aaa ttg aat tgg gcg agt cag				1104
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ggg cac aca acg gaa gct cta tta gat aca gga gca gat gat aca gta				96
Gly His Thr Thr Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	20	25	30	
tta gaa gaa atg aat ttg cca ggg aga tgg aaa cca aaa atg ata gga				144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	35	40	45	
gga att gga ggt ttt atc aaa gta aga cag tat gag cag gta ccc ata				192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Glu Gln Val Pro Ile	50	55	60	
gaa ttc tgt gga cat aaa act gta ggt aca gta tta ata gga cct aca				240
Glu Phe Cys Gly His Lys Thr Val Gly Thr Val Leu Ile Gly Pro Thr	65	70	75	80
cct gtc aac ata att gga aga aat ctg atg act cag att ggt tgt act				288

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tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Pro	Trp	Pro	Leu	Thr	Glu	Arg	
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Lys	Asn	Lys	Ala	Leu	Val	Glu	Ile	Cys	Ser	Glu	Met	Glu	Lys	Gly	Arg	
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Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
				180				185					190			
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Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu	
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Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Glu	Glu	Phe	Arg	
						215					220					
aag	tat	act	gca	ttc	acc	ata	cct	agt	aca	aac	aat	gaa	aca	cca	ggg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Gly	
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
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Gln	Asn	Pro	Glu	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
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Ala	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Val	Glu	Glu	Leu	
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Arg	Gln	His	Leu	Leu	Lys	Trp	Gly	Phe	Phe	Thr	Pro	Asp	Glu	Lys	His	
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cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
					325				330					335		
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Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Asp	Gln	Asp	Ser	Trp	Thr	
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COFFEE

- 143 -

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Gln Asn Pro Asp Ile Val Ile Xaa Xaa Tyr Val Asp Asp Leu Tyr Val				
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gga tct gac tta gaa ata ggg aag cat agg gaa aaa ata gag gaa ctg				912
Gly Ser Asp Leu Glu Ile Gly Lys His Arg Glu Lys Ile Glu Glu Leu				
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aga caa cat ctg tgg aag tgg gga ttt tac aca cca gac gaa aaa cat				960
Arg Gln His Leu Trp Lys Trp Gly Phe Tyr Thr Pro Asp Glu Lys His				
	305	310	315	320
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat ctt gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Leu Asp				
	325	330	335	
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gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag				1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
	355	360	365	
att tat gca ggg				1116
Ile Tyr Ala Gly				
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	1	5	10	15
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta				96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val				
	20	25	30	
tta gaa gaa atg agt ttg cca ggg aga tgg aaa cca aaa atg ata ggg				144
Leu Glu Glu Met Ser Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly				
	35	40	45	
gga att gga ggt ttt atc aaa gta aga caa ttt gat cag ata ccc ata				192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Phe Asp Gln Ile Pro Ile				
	50	55	60	
gaa ata tgt gga cac aaa gct ata ggt aca gta tta ata gga cct aca				240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr				
	65	70	75	80
cct gtc aac ata att gga agg aat ctg ttg act cag ctt ggt tgc act				288

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Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Pro	Val	Pro	Val	Lys	Leu	Lys	
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
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Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Leu	Glu	Lys	Glu	Gly	
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Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
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Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
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Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
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Arg	Glu	His	Leu	Leu	Lys	Trp	Gly	Phe	Tyr	Thr	Pro	Asp	Lys	Lys	His	
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Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
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att tat gca ggg	1116
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gga cag cta aag gaa gct yta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Xaa Leu Asp Thr Gly Ala Asp Asp Thr Val	
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Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Ile Ile Gly	
35 40 45	
gga att gga ggt ttt gtc aga gta aga caa tat gat cag gta cct gta	192
Gly Ile Gly Gly Phe Val Arg Val Arg Gln Tyr Asp Gln Val Pro Val	
50 55 60	
gaa att tgt gga cat aaa gct ata ggt tca gta tta gta gga cca aca	240
Glu Ile Cys Gly His Lys Ala Ile Gly Ser Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gcc aac ata att gga aga aat ctg atg act cag ctt ggt ttc act	288
Pro Ala Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Phe Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
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cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
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Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aag aac agt gat aga tgg aga aaa tta gta gat ttc	528
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gga tct gac cta gaa ata ggg Gly Ser Asp Leu Glu Ile Gly 290 295	cag cat aga aca aaa Gln His Arg Thr Lys 300	ata gag gaa ctg Ile Glu Glu Leu	912
aga caa cat ttg ttg aaa tgg Arg Gln His Leu Leu Lys Trp 305 310	gga ttt atc aca cca Gly Phe Ile Thr Pro 315	gat gaa aaa cat Asp Glu Lys His 320	960
cag aaa gaa cct cca ttc ctt Gln Lys Glu Pro Pro Phe Leu 325	tgg atg ggg tat gaa ctc Trp Met Gly Tyr Glu Leu 330 335	cat cct gat His Pro Asp	1008
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gtc aat gac ata cag aaa tta Val Asn Asp Ile Gln Lys Leu 355	gtg gga aaa ttg aat Val Gly Lys Leu Asn 360 365	tgga gca agt cag Trp Ala Ser Gln	1104
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ggg cag cta aag gaa gct cta tta Gly Gln Leu Lys Glu Ala Leu Leu 20 25	gat aca gga gca gat gat aca gta Thr Gly Ala Asp Asp Thr Val 25 30		96
tta gaa gac ata aac ttg cca gga Leu Glu Asp Ile Asn Leu Pro Gly 35 40	aaa tgg aaa cca aaa atg ata ggg Lys Trp Lys Pro Lys Met Ile Gly 40 45		144
gga att gga ggt ttt atc aaa gta Gly Ile Gly Gly Phe Ile Lys Val 50 55	aga cag tat gag cag gta ccc ata Arg Gln Tyr Glu Gln Val Pro Ile 60		192
gaa atc tgt gga cat aaa act ata Glu Ile Cys Gly His Lys Thr Ile 65 70	ggt aca gta tta gta gga cct aca Gly Thr Val Leu Val Gly Pro Thr 75 80		240
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ggg caa cta ata gag gct cta ttg gat aca gga gca gat gat aca gta Gly Gln Leu Ile Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val 20 25 30	96
tta gaa gaa atg gat ttg cca gga aga tgg aaa cca aaa ata ata ggg Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Lys Pro Lys Ile Ile Gly 35 40 45	144
gga att gga ggt tgg atc aaa gta aga caa tat gat cag ata ccc ata Gly Ile Gly Gly Trp Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile 50 55 60	192
gaa att tgt gga cat aaa gtt ata agt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Val Ile Ser Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cca gtc aac gta att gga aga aat ctg atg act cag att ggt tgc act Pro Val Asn Val Ile Gly Arg Asn Leu Met Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aga gtt aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Arg Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aag ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gat ggg Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa gta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Val Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta ggg Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta cca aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Pro Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aaa tat act gca ttt acc ata cct agt ata aat aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
gtt aga tat cag tac aat gtg ctc cca cag ggg tgg aaa gga tca cca Val Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg acc aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816

Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
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tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
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Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
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Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	
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Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
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Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cat	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
		195				200						205				
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gac	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg	
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Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly	
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
			245						250					255		
gca	ata	ttc	cag	tgt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Cys	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gar	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ctg	tat	gta	864
Gln	Asn	Pro	Glu	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gaa	ata	gaa	cag	cat	aga	ata	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Glu	Gln	His	Arg	Ile	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	cac	cat	ctg	ttg	aaa	tgg	gga	ttt	wmc	aca	cca	gac	aaa	aaa	cat	960
Arg	His	His	Leu	Leu	Lys	Trp	Gly	Phe	Xaa	Thr	Pro	Asp	Lys	Lys	His	
	305				310					315					320	
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggt	tat	gaa	ctc	cat	cct	gat	1008
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	
			325						330					335		
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Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	
			340					345					350			

gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag 1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln
355 360 365

att tac cca ggg 1116
Ile Tyr Pro Gly
370

<210> 96
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<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
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<222> (0)...(297)
<223> HIV Protease

<221> CDS
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<223> Portion of HIV Reverse Transcriptase

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ggg caa cta agg gaa gct cta tta gat aca gga gca gat gat aca gta 96
Gly Gln Leu Arg Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val
20 25 30

tta gaa gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg 144
Leu Glu Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly
35 40 45

gga att ggg ggt ttt atc aaa gta aga sag tat gat cag gta ccc gta 192
Gly Ile Gly Gly Phe Ile Lys Val Arg Xaa Tyr Asp Gln Val Pro Val
50 55 60

gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta gga ccc aca 240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr
65 70 75 80

cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta ara tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Xaa Leu Lys
100 105 110

cca ggr atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Xaa Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125

aaa ata aaa gca tta gta gaa atc tgt aca gaa atg gaa aag gaa ggg 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
130 135 140

aaa att tca aaa att ggg cct gaa aat cca tac aat act cca ata ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe
145 150 155 160

gcc ata aag aaa aaa gac ggt act aaa tgg aga aaa gta gta gat ttc 528
Ala Ile Lys Lys Lys Asp Gly Thr Lys Trp Arg Lys Val Val Asp Phe
165 170 175

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ggg Gly	caa Gln	ata Ile	aag Lys 20	gaa Glu	gcy Xaa	tta Leu	tta Leu	gat Asp 25	aca Thr	gga Gly	gca Ala	gat Asp	gat Asp 30	aca Thr	gtg Val	96	
tta Leu	gaa Glu	gaa Glu 35	atg Met	aat Asn	ttg Leu	cca Pro	gga Gly 40	aaa Lys	tgg Trp	aaa Lys	cca Pro	aaa Lys 45	ttg Leu	ata Ile	ggg Gly	144	
gga Gly	att Ile 50	gga Gly	ggt Gly	ttt Phe	atc Ile	aaa Lys 55	gta Val	aga Arg	cag Gln	tat Tyr	gat Asp 60	cag Gln	ata Ile	ctt Leu	ata Ile	192	
gaa Glu 65	atc Ile	tgt Cys	ggc Gly	cat His	aaa Lys 70	gct Ala	ata Ile	ggg Gly	aca Thr	gta Val 75	tta Leu	gta Val	gga Gly	cct Pro	aca Thr 80	240	
cct Pro	gcc Ala	aac Asn	ata Ile	att Ile 85	gga Gly	aga Arg	aat Asn	ctg Leu	ttg Leu 90	act Thr	cag Gln	att Ile	ggg Gly	tgc Cys 95	act Thr	288	
tta Leu	aat Asn	ttt Phe 100	ccc Pro	att Ile	agt Ser	cct Pro	att Ile	gaa Glu 105	act Thr	gta Val	cca Pro	gta Val	aaa Lys 110	tta Leu	aag Lys	336	
cca Pro	gga Gly 115	atg Met	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384	
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	cta Leu	gaa Glu 135	att Ile	tgt Cys	aca Thr	gaa Glu	ctg Leu 140	gaa Glu	aag Lys	gaa Glu	ggg Gly	432	
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cct Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480	
gcc Ala	ata Ile	aag Lys	aaa Lys 165	aaa Lys	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528	
aga Arg	gaa Glu	ctt Leu 180	aat Asn	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttt Phe	tgg Trp	gag Glu	gtt Val	caa Gln 190	cta Leu	gga Gly	576	
ata Ile	cca Pro	cat His 195	ccc Pro	gsa Xaa	ggg Gly	tta Leu	aga Arg 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624	
gat Asp	gtg Val 210	ggg Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	tat Tyr 220	gag Glu	gac Asp	tty Phe	agg Arg	672	
aaa Lys 225	tat Tyr	act Thr	gca Ala	ttt Phe	act Thr 230	ata Ile	cct Pro	agt Ser	aca Thr	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240	720	
att Ile	agg Arg	tat Tyr	cag Gln	tac Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768	
gca Ala	ata Ile	ttc Phe	caa Gln	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe	aga Arg	aaa Lys	816	

260	265	270	
caa aat cca gac ata gtt atc trt Gln Asn Pro Asp Ile Val Ile Xaa 275 280	caa tac gtg gat gat Gln Tyr Val Asp Asp 285	ttg tat gta Leu Tyr Val	864
gga tct gac tta gaa ata ggg Gly Ser Asp Leu Glu Ile Gly 290 295	cag cat aga aca aaa Gln His Arg Thr Lys 300	ata gag gaa ctg Ile Glu Glu Leu	912
aga caa cat ctg tgg cag tgg Arg Gln His Leu Trp Gln Trp Gly 305 310	ttt ttc aca cca gac Phe Phe Thr Pro Asp 315	aaa aaa cat Lys Lys His 320	960
cag aaa gaa cct cca ttc ctt tgg Gln Lys Glu Pro Pro Phe Leu Trp 325	atg ggt tat gaa ctc cat Met Gly Tyr Glu Leu His 330 335	cct gat Pro Asp	1008
aaa tgg aca gta cag cct ata gta Lys Trp Thr Val Gln Pro Ile Val 340	ctg cca gaa aaa gac agc Leu Pro Glu Lys Asp Ser 345 350	tgg act Trp Thr	1056
gtc aat gac ata cag aag tta gtg Val Asn Asp Ile Gln Lys Leu Val 355 360	gga aaa ttg aat tgg Gly Lys Leu Asn Trp 365	gca agt cag Ala Ser Gln	1104
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ggg caa cta aag gaa gct cta tta gat Gly Gln Leu Lys Glu Ala Leu Leu Asp 20 25	aca gga gca gat gat aca gta Thr Gly Ala Asp Thr Val 30		96
tta gaa gaa atg cat ttg cca gga Leu Glu Glu Met His Leu Pro Gly 35 40	aaa tgg aaa cca aaa atg ata ggg Lys Trp Lys Pro Lys Met Ile Gly 45		144
gga att gga ggt ttt atc aaa gta Gly Ile Gly Gly Phe Ile Lys Val 50 55	aga cag tat gat cag ata cct gta Arg Gln Tyr Asp Gln Ile Pro Val 60		192
gaa aty tgt gga cat aaa gct ata Glu Xaa Cys Gly His Lys Ala Ile 65 70	ggt aca gta tta gta gga cct aca Thr Val Leu Val Gly Pro Thr 75 80		240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act			288

Pro	Val	Asn	Ile	Ile 85	Gly	Arg	Asn	Leu	Leu 90	Thr	Gln	Ile	Gly	Cys 95	Thr	
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cca Pro	ggg Gly	atg Met 115	gat Asp	ggc Gly	cca Pro	aaa Lys	gtt Val 120	aaa Lys	caa Gln	tgg Trp	cca Pro	ttg Leu 125	aca Thr	gaa Glu	gaa Glu	384
aaa Lys	ata Ile 130	aaa Lys	gca Ala	tta Leu	gta Val	gaa Glu 135	ata Ile	tgt Cys	aca Thr	gaa Glu	atg Met 140	gaa Glu	aag Lys	gaa Glu	ggg Gly	432
aaa Lys 145	att Ile	tca Ser	aaa Lys	att Ile	ggg Gly 150	cca Pro	gaa Glu	aat Asn	cca Pro	tac Tyr 155	aat Asn	act Thr	cca Pro	gta Val	ttt Phe 160	480
gcc Ala	ata Ile	aag Lys	aaa Lys	aaa Lys 165	gac Asp	agt Ser	act Thr	aaa Lys	tgg Trp 170	aga Arg	aaa Lys	tta Leu	gta Val	gat Asp 175	ttc Phe	528
aga Arg	gaa Glu	ctt Leu	aat Asn 180	aag Lys	aga Arg	act Thr	caa Gln	gac Asp 185	ttc Phe	tgg Trp	gaa Glu	gtt Val	caa Gln 190	ttg Leu	gga Gly	576
ata Ile	cca Pro	cat His 195	ccc Pro	gca Ala	gga Gly	tta Leu	aaa Lys 200	aag Lys	aaa Lys	aaa Lys	tca Ser	gta Val 205	aca Thr	gta Val	ctg Leu	624
gat Asp	gtg Val 210	ggg Gly	gat Asp	gca Ala	tat Tyr	ttt Phe 215	tca Ser	gtt Val	ccc Pro	tta Leu	gat Asp 220	aaa Lys	gac Asp	ttc Phe	agg Arg	672
aag Lys 225	tac Tyr	act Thr	gca Ala	ttt Phe	acc Thr 230	ata Ile	cct Pro	agt Ser	ata Ile	aac Asn 235	aat Asn	gag Glu	aca Thr	cca Pro	ggg Gly 240	720
att Ile	aga Arg	tat Tyr	cag Gln	tat Tyr 245	aat Asn	gtg Val	ctt Leu	cca Pro	cag Gln 250	gga Gly	tgg Trp	aaa Lys	gga Gly	tca Ser 255	cca Pro	768
gca Ala	ata Ile	ttc Phe	caa Gln 260	agt Ser	agc Ser	atg Met	aca Thr	aaa Lys 265	atc Ile	tta Leu	gag Glu	cct Pro	ttt Phe 270	aga Arg	aaa Lys	816
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gga Gly	tcc Ser 290	gac Asp	cta Leu	gaa Glu	ata Ile	ggg Gly 295	cag Gln	cat His	aga Arg	aca Thr	aaa Lys 300	ata Ile	gag Glu	gaa Glu	ctg Leu	912
aga Arg 305	caa Gln	cac His	ctg Leu	ttg Leu	aag Lys 310	tgg Trp	ggr Xaa	ttt Phe	acc Thr	ack Xaa 315	cca Pro	gac Asp	aaa Lys	aaa Lys	cat His 320	960
cag Gln	aag Lys	gaa Glu	cct Pro	cca Pro 325	ttc Phe	ctt Leu	tgg Trp	atg Met	ggg Gly 330	tat Tyr	gaa Glu	ctc Leu	cat His	cct Pro 335	gat Asp	1008
aaa Lys	tgg Trp	aca Thr	gta Val 340	cag Gln	cct Pro	ata Ile	gta Val 345	ctg Leu	cca Pro	gaa Glu	aaa Lys	gat Asp	agc Ser 350	tgg Trp	act Thr	1056

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1 5 10 15	
ggg cag ctr aag gaa gct ata tta gat aca gga gca gat gat aca kta	96
Gly Gln Xaa Lys Glu Ala Ile Leu Asp Thr Gly Ala Asp Asp Thr Xaa	
20 25 30	
tta gaa gaa atg aat tng ccc gga aga tgg ama cca ama ttg ata ggg	144
Leu Glu Glu Met Asn Xaa Pro Gly Arg Trp Xaa Pro Xaa Leu Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa atc tgt gga cat aaa gtt ata ggt aca gta ttg gta gga cct aca	240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct acc aac ata att gga aga aat ctg atg act cag ctt ggt tgc act	288
Pro Thr Asn Ile Ile Gly Arg Asn Leu Met Thr Gln Leu Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa ggg	432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	
130 135 140	
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt	480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	
145 150 155 160	
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc	528
Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga	576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	
180 185 190	
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca ata ctg	624
Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Ile Leu	
195 200 205	
gat gtg ggc gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aaa gta tac tgc ttt acc ata cct agt ata acc aat gag acm cca ggg	720
Lys Val Tyr Cys Phe Thr Ile Pro Ser Ile Thr Asn Glu Xaa Pro Gly	
225 230 235 240	
att aga tat cag tac aat gtg ctg cca caa gga tgg aaa gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag ccy ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Xaa Phe Arg Lys	

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	275	280	285	
gga tct gac tta gaa ata ggg cag cat aga gca aaa ata gag gaa ctg				912
Gly Ser Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu				
	290	295	300	
aga caa cat ctg tgg agg tgg gga ttt tac aca cca gac aaa aaa cat				960
Arg Gln His Leu Trp Arg Trp Gly Phe Tyr Thr Pro Asp Lys Lys His				
	305	310	315	320
cag aag gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat				1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp				
	325	330	335	
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Lys Trp Thr Val Gln Pro Ile Xaa Leu Pro Glu Lys Asp Ser Trp Thr				
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gtc aat gam ata cag aaa tta gtg gga aaa tta aat tgg gcc agt cag				1104
Val Asn Xaa Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln				
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Ile Xaa Xaa				
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<223> Portion of HIV Reverse Transcriptase				
<400> 101				
cct car atc act ctt tgg cag acc ccc ctt gtc yca ata agg aka ggg				48
Pro Gln Ile Thr Leu Trp Gln Thr Pro Leu Val Xaa Ile Arg Xaa Gly				
	1	5	10	15
ggr cag yta aag gaa gct tta tta gay aca gra gca gat gat mca gta				96
Xaa Gln Xaa Lys Glu Ala Leu Leu Asp Thr Xaa Ala Asp Asp Xaa Val				
	20	25	30	
tta gaa gaa atg tat ttg cca gga aga tgg aaa cca aaa atg ata ggg				144
Leu Glu Glu Met Tyr Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly				
	35	40	45	
gga att gga ggt ttt atc aag gta aga cag tat gat cag ata ccc ata				192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile				
	50	55	60	
gaa atc tgt gga cac aaa gct ata ggt aca gta ttg gta gga tct aca				240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Ser Thr				
	65	70	75	80
cct gtt aac ata att gga aga aat ctg ttg act cag att ggt tgc acc				288

gtc aat gac ata cag aag tta gta gga aaa ttg aat tgg g 1096
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp
355 360 365

<210> 102
<211> 1048
<212> DNA
<213> Human Immunodeficiency Virus (HIV)

<220>
<221> CDS
<222> (0)...(297)
<223> HIV Protease

<221> CDS
<222> (298)...(1048)
<223> Portion of HIV Reverse Transcriptase

<400> 102
cct cag atc act ctt tgg cag cga ccc tty gtc aca ata aag gta ggg 48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Thr Ile Lys Val Gly
1 5 10 15
ggg caa cta aag gaa gct cta ttg gat aca gga gca gat gat aca ata 96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Ile
20 25 30
tta gaa gaa atg tgt ttg cca gga aga tgg aaa cca aaa ttg ata ggg 144
Leu Glu Glu Met Cys Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly
35 40 45
gga att gga ggt ttt gtc aaa gta aga caa tat gat cag ata ccc ata 192
Gly Ile Gly Gly Phe Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
50 55 60
gaa atc tgt gga cat aaa gtt ata ggt aca gta tta gta gga cct aca 240
Glu Ile Cys Gly His Lys Val Ile Gly Thr Val Leu Val Gly Pro Thr
65 70 75 80
cct gcc aac ata gtt gga aga aat ctg ttg act cag att ggc tgt act 288
Pro Ala Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
85 90 95
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
100 105 110
cca gga atg gat ggg cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
115 120 125
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gag aag gat gga 432
Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Asp Gly
130 135 140
aaa att tca aaa att ggg cct gaa aat cca tay aat act cca gta ttt 480
Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
145 150 155 160
gcc ata aag aaa aaa aat agt gat aaa tgg aga aaa gta gta gat ttc 528
Ala Ile Lys Lys Lys Asn Ser Asp Lys Trp Arg Lys Val Val Asp Phe
165 170 175
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga 576
Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
180 185 190

ata cca cat ccc gga ggg tta rag aag aac aaa tca ata aca gta ctg	624
Ile Pro His Pro Gly Gly Leu Xaa Lys Asn Lys Ser Ile Thr Val Leu	
195 200 205	
gat gtg ggt gat gca tat ttt tca att ccc tta gat aaa gac ttc aga	672
Asp Val Gly Asp Ala Tyr Phe Ser Ile Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt acc ata ccy agt ata aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Thr Ile Xaa Ser Ile Asn Asn Glu Thr Pro Gly	
225 230 235 240	
att aga tat cag tat aat gtg ctt cca cag gga tgg aag gga tca cca	768
Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gcc ata ttc caa agt agc atg aca aaa ata tta gag cct ttt aga aag	816
Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca gac ata att atc gtt caa tac gtg gat gat ttg tat gta	864
Gln Asn Pro Asp Ile Ile Ile Val Gln Tyr Val Asp Asp Leu Tyr Val	
275 280 285	
gca tct gac tta gaa ata ggg cag cat aga aca aaa ata aag gaa cta	912
Ala Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Lys Glu Leu	
290 295 300	
aga caa tat ctg tgg gag tgg gga ttt tac aca cca gac aaa aaa cat	960
Arg Gln Tyr Leu Trp Glu Trp Gly Phe Tyr Thr Pro Asp Lys Lys His	
305 310 315 320	
caa cag gaa ccc cca ttc ctc tgg atg ggg tat gag ctc cat cct gat	1008
Gln Gln Glu Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac a	1048
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp	
340 345	
<210> 103	
<211> 1116	
<212> DNA	
<213> Human Immunodeficiency Virus (HIV)	
<220>	
<221> CDS	
<222> (0)...(297)	
<223> HIV Protease	
<221> CDS	
<222> (298)...(1116)	
<223> Portion of HIV Reverse Transcriptase	
<400> 103	
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata arg rta ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Xaa Xaa Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg aat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	

35					40					45						
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	cag	ata	ccc	ata	192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Pro	Ile	
	50					55					60					
gaa	atc	tgt	gga	cat	aaa	gct	gaa	ggt	aca	gta	tta	gta	gga	cct	aca	240
Glu	Ile	Cys	Gly	His	Lys	Ala	Glu	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr	
	65				70				75						80	
ccg	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	att	ggt	tgc	act	288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Ile	Gly	Cys	Thr	
				85				90						95		
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag	336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	
			100					105					110			
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ctg	aca	gaa	gaa	384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	
		115					120					125				
aaa	ata	aaa	gca	tta	aba	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	ggr	432
Lys	Ile	Lys	Ala	Leu	Xaa	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Xaa	
	130					135					140					
aaa	att	tca	aaa	att	ggg	cct	gaa	aat	cca	tac	aat	act	ccg	gta	ttt	480
Lys	Ile	Ser	Lys	Ile	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe	
	145				150					155					160	
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	
				165					170					175		
aga	gaa	ctt	aat	aag	aaa	act	caa	gac	ttt	tgg	gaa	gtt	caa	tta	gga	576
Arg	Glu	Leu	Asn	Lys	Lys	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	
			180					185					190			
ata	cca	cac	ccc	gca	ggg	tta	aaa	aag	aaa	aaa	tca	gta	aca	gta	ctg	624
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Lys	Lys	Ser	Val	Thr	Val	Leu	
			195				200					205				
gat	gtg	ggt	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gaa	ttc	agg	672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg	
	210					215					220					
aag	tat	aca	gca	ttt	acc	ata	cct	agt	aca	aac	aat	gag	aca	ccc	agg	720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Thr	Asn	Asn	Glu	Thr	Pro	Arg	
	225				230					235					240	
att	aga	tat	cag	tac	aat	gtg	ctt	cca	cag	gga	tgg	aaa	gga	tcg	cca	768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	
				245					250					255		
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys	
			260					265					270			
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tat	gtg	gat	gat	ttg	tat	gta	864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Val	Asp	Asp	Leu	Tyr	Val	
		275					280					285				
gga	tct	gac	tta	gag	ata	ggg	cag	cat	aga	aca	aaa	ata	gag	gaa	ctg	912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu	
	290					295					300					
aga	saa	cat	ctg	ttg	agg	tgg	gga	ttt	acc	aca	cca	gac	aaa	aaa	cat	960

[illegible]

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<212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 105
 cct cag atc act ctt tgg caa cga ccc ttc gtc gtc gta aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Phe Val Val Val Lys Ile Gly
 1 5 10 15

ggg caa cta aag gaa gct cta tta gat aca gga gca gat aat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asn Thr Val
 20 25 30

ttt gaa gac ytg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Phe Glu Asp Xaa Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45

gga att gga ggt ttt atc aaa gta aga cag tat gat cag gta ctt gta 192
 Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Val Leu Val
 50 55 60

gaa atc tgt gga caa aaa gct ata ggt aca gta tta ata gga cct aca 240
 Glu Ile Cys Gly Gln Lys Ala Ile Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80

cct gtc aac ata att gga agg gat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

aar att tca aaa att ggg cct gaa aac cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

gcc ata aag aaa aaa gac agt act aar tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gay ttc agg 672
 Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg

210	215	220	
aag tat act gca ttt acc ata cct agc ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa tgt agc atg aca aaa atc tta gat cct ttt aga aag Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Asp Pro Phe Arg Lys 260 265 270			816
caa aat cca gac cta gtt atc tat caa tac rtg gat gac ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Tyr Val 275 280 285			864
gga tct gat tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300			912
aga car cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aar cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gtg ctg cca gaa aag gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tac cca ggg Ile Tyr Pro Gly 370			1116

<210> 106
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 106 cct cag atc act ctt ngg caa cga ccm att gtc aca ata aag gta ggg Pro Gln Ile Thr Leu Xaa Gln Arg Xaa Ile Val Thr Ile Lys Val Gly 1 5 10 15	48
ggg cam tta aaa gaa gtt ytt tta gat mma gga gca gat gat cma gta Gly Xaa Leu Lys Glu Val Xaa Leu Asp Xaa Gly Ala Asp Asp Xaa Val 20 25 30	96
tta gaa gaa atr gat ttg cca gga aga tgg aaa cca aaa atg ata ggg	144

Leu	Glu	Glu	Xaa	Asp	Leu	Pro	Gly	Arg	Trp	Lys	Pro	Lys	Met	Ile	Gly		
		35					40					45					
gga	att	gga	ggt	ttt	atc	aaa	gta	aga	cag	tat	gat	caa	ata	gtt	gta		192
Gly	Ile	Gly	Gly	Phe	Ile	Lys	Val	Arg	Gln	Tyr	Asp	Gln	Ile	Val	Val		
	50					55					60						
gaa	atc	tgt	gga	cat	aaa	gct	ata	ggt	aca	gta	tta	gta	gga	cct	aca		240
Glu	Ile	Cys	Gly	His	Lys	Ala	Ile	Gly	Thr	Val	Leu	Val	Gly	Pro	Thr		
	65				70					75					80		
cct	gtc	aac	ata	att	gga	aga	aat	ctg	ttg	act	cag	ctt	ggt	tgc	act		288
Pro	Val	Asn	Ile	Ile	Gly	Arg	Asn	Leu	Leu	Thr	Gln	Leu	Gly	Cys	Thr		
				85					90					95			
tta	aat	ttt	ccc	att	agt	cct	att	gaa	act	gta	cca	gta	aaa	tta	aag		336
Leu	Asn	Phe	Pro	Ile	Ser	Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys		
			100					105					110				
cca	gga	atg	gat	ggc	cca	aaa	gtt	aaa	caa	tgg	cca	ttg	aca	gag	gaa		384
Pro	Gly	Met	Asp	Gly	Pro	Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	ttg	gta	gaa	att	tgt	aca	gaa	atg	gaa	aag	gaa	gga		432
Lys	Ile	Lys	Ala	Leu	Val	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly		
	130					135					140						
aaa	att	tca	aaa	aty	ggg	cct	gaa	aat	cca	tac	aat	act	cca	gta	ttt		480
Lys	Ile	Ser	Lys	Xaa	Gly	Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
	145				150					155					160		
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc		528
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165					170					175			
agg	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	gtt	caa	tta	gga		576
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
			180					185					190				
ata	cca	cat	ccc	gca	ggg	yta	aaa	aag	aac	aaa	tca	gta	aca	gta	ctg		624
Ile	Pro	His	Pro	Ala	Gly	Xaa	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu		
			195				200					205					
gat	gtg	ggt	gat	gca	tat	ttc	tca	gtt	ccc	tta	gat	aaa	gac	ttt	agg		672
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Asp	Phe	Arg		
	210					215					220						
aag	tat	act	gca	ttt	acc	ata	ccc	agt	ata	aac	aat	gag	aca	cca	ggg		720
Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
	225				230					235					240		
att	aga	tat	cag	tat	aat	gtg	ctt	cca	caa	gga	tgg	aaa	gga	tca	cca		768
Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro		
				245					250					255			
gca	ata	ttc	caa	agt	agc	atg	aca	aaa	atc	cta	gag	cct	ttt	agg	aaa		816
Ala	Ile	Phe	Gln	Ser	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
			260					265					270				
caa	aat	cca	gac	ata	gtt	atc	tat	caa	tac	atg	gat	gat	ttg	tat	gta		864
Gln	Asn	Pro	Asp	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
		275					280					285					
gga	tct	gac	tta	gaa	ata	ggg	cag	cat	aga	aca	aaa	ata	gaa	gaa	ctg		912
Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu		
	290					295					300						

aga gca cat ctg tta aag tgg gga ttt acc aca cca gay aaa aag cat	960
Arg Ala His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aaa gaa cct cca ttt ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gtg cag cct ata aag ctg cca gaa aaa gac agc tgg act	1056
Lys Trp Thr Val Gln Pro Ile Lys Leu Pro Glu Lys Asp Ser Trp Thr	
340 345 350	
gtc aat gat ata cag aag tta gtg gga aaa ttg aat tgg gcc agt cag	1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tat cca gga	1116
Ile Tyr Pro Gly	
370	

<210> 107
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 107	
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg caa cta aag gaa gct tta tta gat aca gga gca gat gat aca gta	96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	
tta gaa gaa atg gaa ttg cca gga aga tgg aaa cca aaa atg ata ggg	144
Leu Glu Glu Met Glu Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	
35 40 45	
gga att gga ggt ttt atc aaa gta agm cag tat gat cag ata ccc ata	192
Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Asp Gln Ile Pro Ile	
50 55 60	
gaa att tgt gga cat aaa gct gtg ggt aca gta tta gta gga cct aca	240
Glu Ile Cys Gly His Lys Ala Val Gly Thr Val Leu Val Gly Pro Thr	
65 70 75 80	
cct gtc aac ata att gga aga aat ctg ttg act aag att ggt tgc act	288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Lys Ile Gly Cys Thr	
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag	336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa	384
Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	
115 120 125	

aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att gga cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Glu Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa mgg aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Xaa Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gag ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Glu Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag aca cca gga Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg yyt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Xaa Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gaa ata gtt atc tat cag tac atg gat gat ttg tat gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cac aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu 290 295 300	912
aga caa cat ctg ttg aag tgg gga ttt acc aca cca gac aaa aaa cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320	960
cag aaa gaa ccc cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335	1008
aaa tgg aca gta cag cct ata gtg cta cca gaa aaa gac agc tgg act Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr 340 345 350	1056
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gcg agt cag Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365	1104
att tay gca ggg Ile Tyr Ala Gly 370	1116

<210> 108

<211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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 Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly
 1 5 10 15

 ggg cag cta aag gaa gct cta tta gat aca gga gca gat gat aca gtg 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val
 20 25 30

 tta gaa gaa atg aat ttg cca ggg aaa tgg aag cca aaa atg ata ggg 144
 Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45

 gga att gga ggg ttt atc aaa gta agm crg tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Xaa Xaa Tyr Asp Gln Ile Pro Ile
 50 55 60

 gaa atc tgt gra cat aaa gct aya ggt aca gta tta ata ggm cct act 240
 Glu Ile Cys Xaa His Lys Ala Xaa Gly Thr Val Leu Ile Xaa Pro Thr
 65 70 75 80

 cct gtc aac ata att gga aga awt ctg atg act cag att ggg tgc act 288
 Pro Val Asn Ile Ile Gly Arg Xaa Leu Met Thr Gln Ile Gly Cys Thr
 85 90 95

 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gag 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aag gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

 aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

 gct ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

 ata cca cat cct gca ggt tta aaa aag aaa aaa tca gta aca gta cta 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

 gat gtg ggg gat gca tat ttt tca gtt ccc tta gat gaa aac ttc agg 672

ttg gam gaa ata aat ttg cca gga aga tgg aaa cca aaa atg ata ggg Leu Xaa Glu Ile Asn Leu Pro Gly Arg Trp Lys Pro Lys Met Ile Gly	144
35 40 45	
gga att gra ggt ttt atc aaa gta aam cag tat gat sag ata mcc ata Gly Ile Xaa Gly Phe Ile Lys Val Xaa Gln Tyr Asp Xaa Ile Xaa Ile	192
50 55 60	
gac atc tgt gga cat aaa gta ata ggt aca ata tta gta gga cct aca Asp Ile Cys Gly His Lys Val Ile Gly Thr Ile Leu Val Gly Pro Thr	240
65 70 75 80	
cct gtc aac ata att gga aga gat ctg ttg act cag att ggc tgc act Pro Val Asn Ile Ile Gly Arg Asp Leu Leu Thr Gln Ile Gly Cys Thr	288
85 90 95	
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys	336
100 105 110	
cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gar gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu	384
115 120 125	
aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly	432
130 135 140	
aag att tca aaa att ggg cct gaa aat cca tac aac act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe	480
145 150 155 160	
gcc ata aag aaa aag gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe	528
165 170 175	
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly	576
180 185 190	
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu	624
195 200 205	
gat gtg ggt gat gca tat tty tca gtt ccc tta gmt aaa gaa tnn nnn Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Xaa Lys Glu Xaa Xaa	672
210 215 220	
nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa	720
225 230 235 240	
nnn nnn nnn nnn nnn nnn nnn nnn cca cag gga tgg aaa gga tca cca Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Gln Gly Trp Lys Gly Ser Pro	768
245 250 255	
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys	816
260 265 270	
caa aat cca gaa ata gtt atc tac car tac rtg gat gay ttg ttw gta Gln Asn Pro Glu Ile Val Ile Tyr Gln Tyr Xaa Asp Asp Leu Xaa Val	864
275 280 285	
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	912
290 295 300	

115	120	125	
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aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160			480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175			528
aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190			576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gtg aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205			624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220			672
aag tac act gca ttt mcc ata cct agt ata aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly 225 230 235 240			720
att aga tat cag tac aat gtg ctt cca caa gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255			768
gca ata ttc caa agt agc atg aca aaa atc tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270			816
caa mat cca gac atg gty atc tat caa tac atg gat gat ttg tat gta Gln Xaa Pro Asp Met Xaa Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285			864
gga tct gac tta gaa ata ggr cag cat aga gca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Xaa Gln His Arg Ala Lys Ile Glu Glu Leu 290 295 300			912
aga cag cat ttg ttg aag tgg gga ttt acc aca cca gac aaa aag cat Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His 305 310 315 320			960
cag aaa gag cct cca ttc ctt tgg atg ggt tat gaa ctc cat cct gat Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp 325 330 335			1008
aaa tgg aca gta cag cct ata gag ctg cca gaa aar gam agc tgg act Lys Trp Thr Val Gln Pro Ile Glu Leu Pro Glu Lys Xaa Ser Trp Thr 340 345 350			1056
gtc aat gac ata cag aaa ata gtg gga aaa ttg aat tgg gca agt cag Val Asn Asp Ile Gln Lys Ile Val Gly Lys Leu Asn Trp Ala Ser Gln 355 360 365			1104
att tac cca ggg Ile Tyr Pro Gly 370			1116

<210> 111
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

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 1 5 10 15
 ggg caa ata aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Ile Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val
 20 25 30
 tta gaa gaa atg agc ttg cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Ser Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ttt atc aaa gta agm cag tat gwt cat ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Xaa His Ile Pro Ile
 50 55 60
 gaa wtc tgt ggm cat aaa gct gaa ggt aca gta tta ata gga cct aca 240
 Glu Xaa Cys Xaa His Lys Ala Glu Gly Thr Val Leu Ile Gly Pro Thr
 65 70 75 80
 cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
 85 90 95
 tta aat ttt ccc ata agt cct att gaa act gta cca gta aga cta aaa 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Arg Leu Lys
 100 105 110
 cca gga atg gat ggg cca aaa gtt aag caa tgg cca cta aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa atc aaa gca ttg ata gaa att tgt aca gaa atg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Ile Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140
 aaa att gaa aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Glu Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata agg aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Arg Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aag aga act caa gac ttt tgg gaa att caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Ile Gln Leu Gly
 180 185 190
 ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta ctg 624
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 195 200 205

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<210> 112
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gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctt gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Val 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt aca gta tta gta gga cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Gly Pro Thr 65 70 75 80	240
cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gag act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtc aaa caa tgg cca ttg aca gaa gaa Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta atg gaa att tgt gca gaa wtg gaa aag gaa gga Lys Ile Lys Ala Leu Met Glu Ile Cys Ala Glu Xaa Glu Lys Glu Gly 130 135 140	432
aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agc act aaa tgg ara aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Xaa Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aar aga act caa gac ttt tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat ccc gca ggg tta aaa aag aaa aaa tca gta aca gta cta Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttc agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aag tat act gca ttt acc ata cct agt ata aac aat gag acm cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Xaa Pro Gly 225 230 235 240	720
att aga tat cag tac aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa agt agc atg aca aaa att tta gag cct ttt aga aaa Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac ata gtt atc tat caa tac atg gat gat ttg tat gta Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	912

290	295	300	
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Arg Gln His Leu Leu Lys Trp Gly Xaa Xaa Thr Pro Asp Lys Lys His			
305	310	315	320
cag aaa saa cct cca ttc ctt tgg atg ggt tat gaa ctc cmt cct gat			1008
Gln Lys Xaa Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu Xaa Pro Asp			
	325	330	335
aaa tgg aca gta caa cct ata gtg ctg cca gaa aag gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
	340	345	350
gtc aat gac ata cag aag tta gtg gga aaa ttr aat tgg gca agt cag			1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Xaa Asn Trp Ala Ser Gln			
	355	360	365
att tac gca ggg			1116
Ile Tyr Ala Gly			
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<223> Portion of HIV Reverse Transcriptase			
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Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly			
1	5	10	15
ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta			96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
	20	25	30
tta gaa gaa atg aat ttg cca gga aaa tgg aaa cca aaa atg ata ggg			144
Leu Glu Glu Met Asn Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly			
	35	40	45
gga att gga ggt ttt atc aaa gta aga cag tat gat cag ata ctc ata			192
Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Ile Leu Ile			
	50	55	60
gaa atc tgt gga cat aaa act ata ggt aca gta tta ata gga cct aca			240
Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Ile Gly Pro Thr			
	65	70	75
cct gtc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act			288
Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr			
	85	90	95
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
	100	105	110
cca gga atg gat ggt cca aga gtt aaa caa tgg cca ttg acm gaa gaa			384

Pro	Gly	Met	Asp	Gly	Pro	Arg	Val	Lys	Gln	Trp	Pro	Leu	Xaa	Glu	Glu		
		115					120					125					
aaa	ata	aaa	gca	tta	ata	gaa	atc	tgc	aca	gaa	atg	gaa	aag	gam	sga	432	
Lys	Ile	Lys	Ala	Leu	Ile	Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Xaa	Xaa		
	130					135					140						
waa	att	tca	aaa	mta	ggg	cct	gam	wat	cca	tac	aat	act	cca	gta	ttt	480	
Xaa	Ile	Ser	Lys	Xaa	Gly	Pro	Xaa	Xaa	Pro	Tyr	Asn	Thr	Pro	Val	Phe		
	145				150					155					160		
gcc	ata	aag	aaa	aaa	gac	agt	act	aaa	tgg	aga	aaa	tta	gta	gat	ttc	528	
Ala	Ile	Lys	Lys	Lys	Asp	Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe		
				165					170					175			
aga	gaa	ctt	aat	aag	aga	act	caa	gac	ttc	tgg	gaa	ggt	caa	tta	gga	576	
Arg	Glu	Leu	Asn	Lys	Arg	Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly		
			180					185					190				
ata	cca	cac	ccg	gca	ggg	tta	aaa	aag	aac	aaa	tca	gta	aca	gtg	ttg	624	
Ile	Pro	His	Pro	Ala	Gly	Leu	Lys	Lys	Asn	Lys	Ser	Val	Thr	Val	Leu		
		195					200					205					
gat	gtg	ggg	gat	gca	tat	ttt	tca	gtt	ccc	tta	gat	aaa	gag	ttc	agg	672	
Asp	Val	Gly	Asp	Ala	Tyr	Phe	Ser	Val	Pro	Leu	Asp	Lys	Glu	Phe	Arg		
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Lys	Tyr	Thr	Ala	Phe	Thr	Ile	Pro	Ser	Ile	Asn	Asn	Glu	Thr	Pro	Gly		
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Ile	Arg	Tyr	Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro		
			245						250					255			
gca	ata	ttc	caa	tst	agc	atg	aca	aaa	atc	tta	gag	cct	ttt	aga	aaa	816	
Ala	Ile	Phe	Gln	Xaa	Ser	Met	Thr	Lys	Ile	Leu	Glu	Pro	Phe	Arg	Lys		
			260					265					270				
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Gln	Asn	Pro	Glu	Ile	Val	Ile	Cys	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val		
		275					280					285					
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Gly	Ser	Asp	Leu	Glu	Ile	Gly	Gln	His	Arg	Thr	Lys	Ile	Glu	Glu	Leu		
	290					295					300						
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Arg	Glu	His	Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His		
	305				310				315						320		
cag	aaa	gaa	cct	cca	ttc	ctt	tgg	atg	ggg	tat	gag	ctc	cat	cct	gat	1008	
Gln	Lys	Glu	Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp		
			325						330					335			
aaa	tgg	aca	gta	cag	cct	ata	gtg	ctg	cca	gaa	aaa	gac	agc	tgg	act	1056	
Lys	Trp	Thr	Val	Gln	Pro	Ile	Val	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr		
			340					345					350				
gtc	aat	gac	ata	cag	aag	tta	gtg	gga	aaa	ttg	aat	tgg	gca	agt	cag	1104	
Val	Asn	Asp	Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln		
		355					360					365					
att	tat	gca	ggg													1116	
Ile	Tyr	Ala	Gly														
	370																

<210> 114
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

 <220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

 <221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 114
 cmt caa atm amt ctt tgg car mra ccc cta gtc cna awn nmm gkk agg 48
 Xaa Gln Xaa Xaa Leu Trp Gln Xaa Pro Leu Val Xaa Xaa Xaa Xaa Arg
 1 5 10 15

 ggg gca aat aag gaa gct cta tta gac aca gga gca gat gat mca gta 96
 Gly Ala Asn Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Xaa Val
 20 25 30

 tta gaa gaa atg wat tta cca gga aaa tgg aaa cca aaa atg ata ggg 144
 Leu Glu Glu Met Xaa Leu Pro Gly Lys Trp Lys Pro Lys Met Ile Gly
 35 40 45

 gga att gga ggt ttt atc aaa gta agn cag tat gag cag ata ccc ata 192
 Gly Ile Gly Gly Phe Ile Lys Val Xaa Gln Tyr Glu Gln Ile Pro Ile
 50 55 60

 gaa atc tgt gga cat aaa gct ata ggt aca gta ttg gta ggm cct aca 240
 Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr
 65 70 75 80

 cct gtc aac ata att gga aga aat ctg ttg act cag att ggt tgc act 288
 Pro Val Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr
 85 90 95

 tta aat ttt ccc att agt cct att gaa act gta cca gtg aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110

 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca tta aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125

 aaa ata aaa gca tta gta gaa att tgt aca gaa atg gaa aaa gaa ggg 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly
 130 135 140

 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160

 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175

 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtc caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190

 ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gtg ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

gac gtg ggt gat gca tat ttt tca gtt ccc tta gat aaa gac ttc agg	672
Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Lys Asp Phe Arg	
210 215 220	
aag tat act gca ttt tcy ata cct agt aca aac aat gag aca cca ggg	720
Lys Tyr Thr Ala Phe Xaa Ile Pro Ser Thr Asn Asn Glu Thr Pro Gly	
225 230 235 240	
agt agg tat caa tac aat gtg ctt cca cag gga tgg aaa gga tca cca	768
Ser Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro	
245 250 255	
gca ata ttc caa agt agc atg ata aaa atc tta gag cct ttt aga aaa	816
Ala Ile Phe Gln Ser Ser Met Ile Lys Ile Leu Glu Pro Phe Arg Lys	
260 265 270	
caa aat cca raa att gtg atc tat cma tac mtg gat gat ttg tat gta	864
Gln Asn Pro Xaa Ile Val Ile Tyr Xaa Tyr Xaa Asp Asp Leu Tyr Val	
275 280 285	
gga tct gac tta gaa ata gaa cag cat aga aca aaa ata gag gaa ctg	912
Gly Ser Asp Leu Glu Ile Glu Gln His Arg Thr Lys Ile Glu Glu Leu	
290 295 300	
aga caa cat ctg ttg agg tgg gga ttt acc aca cca gac aag aaa cat	960
Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys Lys His	
305 310 315 320	
cag aar gaa cct ccg ttc ctt tgg atg ggt tat gaa ctc cat cct gat	1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp	
325 330 335	
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac ags ttg rct	1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Xaa Leu Xaa	
340 345 350	
kca aat gac ata cag aag tta gtg gga aaa ttg aat tgg gca agt cag	1104
Xaa Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln	
355 360 365	
att tac tca ggg	1116
Ile Tyr Ser Gly	
370	

<210> 115
 <211> 1116
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1116)
 <223> Portion of HIV Reverse Transcriptase

<400> 115	
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg	48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly	
1 5 10 15	
ggg cag cta aag gaa gct cta ata gat aca gga gca gat gat aca gtg	96
Gly Gln Leu Lys Glu Ala Leu Ile Asp Thr Gly Ala Asp Asp Thr Val	
20 25 30	

tta gaa gaa atg agt ata cca gga aaa tgg aaa cca aaa ttg ata ggg Leu Glu Glu Met Ser Ile Pro Gly Lys Trp Lys Pro Lys Leu Ile Gly 35 40 45	144
gga att gga ggt ttt atc aaa gta aga cag tat gat cag gkg ccc gta Gly Ile Gly Gly Phe Ile Lys Val Arg Gln Tyr Asp Gln Xaa Pro Val 50 55 60	192
gaa att tgt gga cat aaa gct ata ggt mca gtw tta ata ggm cct aca Glu Ile Cys Gly His Lys Ala Ile Gly Xaa Xaa Leu Ile Xaa Pro Thr 65 70 75 80	240
cct gcc aac ata att gga agg aat ctg ttg act cag att ggt tgc act Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Ile Gly Cys Thr 85 90 95	288
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys 100 105 110	336
cca gga atg gat ggc cca aaa gtt aag caa tgg cca ttg aca gaa gag Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu 115 120 125	384
aaa ata aaa gca tta aca gaa att tgt aca gaa atg gaa aag gaa gga Lys Ile Lys Ala Leu Thr Glu Ile Cys Thr Glu Met Glu Lys Glu Gly 130 135 140	432
aag att tca aaa att ggg cct gaa aat cca tac aat act cca gta ttt Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe 145 150 155 160	480
gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe 165 170 175	528
aga gaa ctt aat aag aga act caa gat ttc tgg gaa gtt caa tta gga Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly 180 185 190	576
ata cca cat cct gca ggg tta aaa aag aaa aaa tca gta aca gta ctg Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu 195 200 205	624
gat gtg ggt gat gca tat ttt tca gtt ccc tta gat gaa gac ttt agg Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg 210 215 220	672
aaa tat act gca ttt acc ata cct agt gta aac aat gag aca cca ggg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Val Asn Asn Glu Thr Pro Gly 225 230 235 240	720
att aga tat cag tat aat gtg ctt cca cag gga tgg aaa gga tca cca Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro 245 250 255	768
gca ata ttc caa tgt agt atg aca aaa ata tta gag ccc ttt aga aaa Ala Ile Phe Gln Cys Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys 260 265 270	816
caa aat cca gac cta gtt atc tat caa tac gtg gat gat ttg tat gta Gln Asn Pro Asp Leu Val Ile Tyr Gln Tyr Val Asp Asp Leu Tyr Val 275 280 285	864
gga tct gac tta gaa ata ggg cag cat aga aca aaa ata gag gaa ctg Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu	912

290	295	300	
aga caa cat ctg ttg aaa tgg ggt ttt acc aca cca gac aaa aag cat			960
Arg Gln His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His			
305	310	315	320
cag aaa gaa cct cca ttc ctt tgg atg ggt tat gaa ctc cat cca gat			1008
Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp			
	325	330	335
aaa tgg aca gta cag cct ata gtg ctg cca gaa aaa gac agc tgg act			1056
Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr			
	340	345	350
gtc aat gac ata cag aag tta gtg gga aaa tta aat tgg gca agt cag			1104
Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln			
	355	360	365
att tac cca ggg			1116
Ile Tyr Pro Gly			
370			
<210> 116			
<211> 1116			
<212> DNA			
<213> Human Immunodeficiency Virus (HIV)			
<220>			
<221> CDS			
<222> (0)...(297)			
<223> HIV Protease			
<221> CDS			
<222> (298)...(1116)			
<223> Portion of HIV Reverse Transcriptase			
<400> 116			
cct cag atc act ctt tgg caa cga ccc ctc gtc aca ata aag ata ggg			48
Pro Gln Ile Thr Leu Trp Gln Arg Pro Leu Val Thr Ile Lys Ile Gly			
1	5	10	15
ggg cag cta aag gaa gct cta tta gat aca gga gca gat gac aca gta			96
Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Asp Thr Val			
	20	25	30
tta gaa gaa ata agt ctg cca gga aga tgg aaa cca aaa ttg ata ggg			144
Leu Glu Glu Ile Ser Leu Pro Gly Arg Trp Lys Pro Lys Leu Ile Gly			
	35	40	45
gga att gga ggt ttt atc aaa gta aag cag tat gat cag ata ccc ata			192
Gly Ile Gly Gly Phe Ile Lys Val Lys Gln Tyr Asp Gln Ile Pro Ile			
50	55	60	
gaa atc tgt gga cat aaa gct ata ggt aca gta tta gta ggm cct aca			240
Glu Ile Cys Gly His Lys Ala Ile Gly Thr Val Leu Val Xaa Pro Thr			
65	70	75	80
cct gtc aac ata gtt gga aga aat ctg ttg act cag ctt ggt tgc act			288
Pro Val Asn Ile Val Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr			
	85	90	95
tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag			336
Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys			
	100	105	110
cca gga atg gat ggc cca aag gtt aag caa tgg cca ttg aca gaa gaa			384

<210> 117
 <211> 1119
 <212> DNA
 <213> Human Immunodeficiency Virus (HIV)

<220>
 <221> CDS
 <222> (0)...(297)
 <223> HIV Protease

<221> CDS
 <222> (298)...(1119)
 <223> Portion of HIV Reverse Transcriptase

<400> 117
 cct caa atc act ctt tgg caa cga ccc atc gtc aca ata aag ata ggg 48
 Pro Gln Ile Thr Leu Trp Gln Arg Pro Ile Val Thr Ile Lys Ile Gly
 1 5 10 15
 ggg caa cta aag gaa gct cta tta gat aca gga gca gat gat aca gta 96
 Gly Gln Leu Lys Glu Ala Leu Leu Asp Thr Gly Ala Asp Thr Val
 20 25 30
 tta gaa gaa atg gat ttg cca gga aga tgg aca cca aaa atg ata ggg 144
 Leu Glu Glu Met Asp Leu Pro Gly Arg Trp Thr Pro Lys Met Ile Gly
 35 40 45
 gga att gga ggt ctt gtc aaa gta aga cag tat gat cag ata ccc ata 192
 Gly Ile Gly Gly Leu Val Lys Val Arg Gln Tyr Asp Gln Ile Pro Ile
 50 55 60
 gaa atc tgt gga cat aaa act ata ggt aca gta tta gta gga cct aca 240
 Glu Ile Cys Gly His Lys Thr Ile Gly Thr Val Leu Val Gly Pro Thr
 65 70 75 80
 cct gcc aac ata att gga aga aat ctg ttg act cag ctt ggt tgt act 288
 Pro Ala Asn Ile Ile Gly Arg Asn Leu Leu Thr Gln Leu Gly Cys Thr
 85 90 95
 tta aat ttt ccc att agt cct att gaa act gta cca gta aaa tta aag 336
 Leu Asn Phe Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys
 100 105 110
 cca gga atg gat ggc cca aaa gtt aaa caa tgg cca ttg aca gaa gaa 384
 Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu
 115 120 125
 aaa ata aaa gca tta gta gaa att tgt aca gaa ttg gaa aag gaa gga 432
 Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Leu Glu Lys Glu Gly
 130 135 140
 aaa att tca aaa att ggg cct gaa aat cca tac aat act cca gtg ttt 480
 Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe
 145 150 155 160
 gcc ata aag aaa aaa gac agt act aaa tgg aga aaa tta gta gat ttc 528
 Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe
 165 170 175
 aga gaa ctt aat aag aga act caa gac ttc tgg gaa gtt caa tta gga 576
 Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly
 180 185 190
 ata cca cat cct gca gga tta aaa aag aaa aaa tca gta aca gta ctg 624
 Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu
 195 200 205

[illegible]

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<210> 118
<211> 979
<212> PRT
<213> Human Immunodeficiency Virus
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Ala	Phe	Thr	Ile	Pro	Ser	Arg	Asn	Asn	Glu	Thr	Pro	Gly	Ile	Arg	Tyr
	130					135					140				
Gln	Tyr	Asn	Val	Leu	Pro	Gln	Gly	Trp	Lys	Gly	Ser	Pro	Ala	Ile	Phe
145					150					155					160
Gln	Ser	Ser	Met	Thr	Arg	Ile	Leu	Glu	Pro	Phe	Arg	Lys	Gln	Asn	Pro
			165						170					175	
Glu	Ile	Val	Ile	Tyr	Gln	Tyr	Met	Asp	Asp	Leu	Tyr	Val	Gly	Ser	Asp
			180					185					190		
Leu	Glu	Ile	Gly	Gln	His	Arg	Ala	Lys	Ile	Glu	Glu	Leu	Arg	Gly	His
	195						200					205			
Leu	Leu	Lys	Trp	Gly	Phe	Thr	Thr	Pro	Asp	Lys	Lys	His	Gln	Lys	Glu
210					215						220				
Pro	Pro	Phe	Leu	Trp	Met	Gly	Tyr	Glu	Leu	His	Pro	Asp	Lys	Trp	Thr
225					230					235					240
Val	Gln	Pro	Ile	Lys	Leu	Pro	Glu	Lys	Asp	Ser	Trp	Thr	Val	Asn	Asp
				245					250					255	
Ile	Gln	Lys	Leu	Val	Gly	Lys	Leu	Asn	Trp	Ala	Ser	Gln	Ile	Tyr	Ala
			260					265					270		
Gly	Ile	Lys	Val	Arg	Gln	Leu	Cys	Lys	Leu	Leu	Arg	Gly	Thr	Lys	Ala
	275						280					285			
Leu	Thr	Glu	Val	Ile	Pro	Leu	Thr	Glu	Glu	Ala	Glu	Leu	Glu	Leu	Ala
	290					295					300				
Glu	Asn	Arg	Glu	Ile	Leu	Lys	Glu	Pro	Val	His	Gly	Val	Tyr	Tyr	Asp
305					310					315					320
Pro	Ser	Lys	Asp	Leu	Ile	Ala	Glu	Ile	Gln	Lys	Gln	Gly	Gln	Gly	Gln
				325					330					335	
Trp	Thr	Tyr	Gln	Ile	Tyr	Gln	Glu	Pro	Phe	Lys	Asn	Leu	Lys	Thr	Gly
			340					345					350		
Lys	Tyr	Ala	Arg	Met	Arg	Gly	Ala	His	Thr	Asn	Asp	Val	Lys	Gln	Leu
	355						360					365			
Thr	Glu	Ala	Val	Gln	Lys	Ile	Thr	Thr	Glu	Ser	Ile	Val	Ile	Trp	Gly
	370					375					380				
Lys	Thr	Pro	Lys	Phe	Lys	Leu	Pro	Ile	Gln	Lys	Glu	Thr	Trp	Glu	Thr
385					390					395					400
Trp	Trp	Thr	Glu	Tyr	Trp	Gln	Ala	Thr	Trp	Ile	Pro	Glu	Trp	Glu	Phe
				405					410					415	
Val	Asn	Thr	Pro	Pro	Leu	Val	Lys	Leu	Trp	Tyr	Gln	Leu	Glu	Lys	Glu
			420					425					430		
Pro	Ile	Val	Gly	Ala	Glu	Thr	Phe	Tyr	Val	Asp	Gly	Ala	Ala	Asn	Arg
	435						440					445			
Glu	Thr	Lys	Leu	Gly	Lys	Ala	Gly	Tyr	Val	Thr	Asn	Arg	Gly	Arg	Gln
	450					455					460				
Lys	Val	Val	Thr	Leu	Thr	Asp	Thr	Thr	Asn	Gln	Lys	Thr	Glu	Leu	Gln
465					470					475					480
Ala	Ile	Tyr	Leu	Ala	Leu	Gln	Asp	Ser	Gly	Leu	Glu	Val	Asn	Ile	Val
				485					490					495	
Thr	Asp	Ser	Gln	Tyr	Ala	Leu	Gly	Ile	Gln	Ala	Gln	Pro	Asp	Gln	
			500					505					510		
Ser	Glu	Ser	Glu	Leu	Val	Asn	Gln	Ile	Ile	Glu	Gln	Leu	Ile	Lys	Lys
	515						520					525			
Glu	Lys	Val	Tyr	Leu	Ala	Trp	Val	Pro	Ala	His	Lys	Gly	Ile	Gly	Ser
	530					535					540				
Pro	Ile	Glu	Thr	Val	Pro	Val	Lys	Leu	Lys	Pro	Gly	Met	Asp	Gly	Pro
545					550					555					560
Lys	Val	Lys	Gln	Trp	Pro	Leu	Thr	Glu	Glu	Lys	Ile	Lys	Ala	Leu	Val
				565					570					575	
Glu	Ile	Cys	Thr	Glu	Met	Glu	Lys	Glu	Gly	Lys	Ile	Ser	Lys	Ile	Gly
			580					585					590		
Pro	Glu	Asn	Pro	Tyr	Asn	Thr	Pro	Ile	Phe	Ala	Ile	Lys	Lys	Lys	Asp
	595						600					605			
Ser	Thr	Lys	Trp	Arg	Lys	Leu	Val	Asp	Phe	Arg	Glu	Leu	Asn	Lys	Arg
	610					615					620				
Thr	Gln	Asp	Phe	Trp	Glu	Val	Gln	Leu	Gly	Ile	Pro	His	Pro	Ala	Gly
625					630					635					640
Leu	Lys	Gln	Lys	Lys	Ser	Val	Thr	Ile	Leu	Asp	Val	Gly	Asp	Ala	Tyr
				645					650					655	
Phe	Ser	Val	Pro	Leu	Asp	Glu	Gly	Phe	Arg	Lys	Tyr	Thr	Ala	Phe	Thr

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Ile	Pro	Ser	660	Arg	Asn	Asn	Glu	Thr	665	Pro	Gly	Ile	Arg	Tyr	670	Gln	Tyr	Asn
Val	Leu	Pro	675	Gln	Gly	Trp	Lys	Gly	680	Ser	Pro	Ala	Ile	Phe	685	Gln	Ser	Ser
Met	Thr	Arg	690	Ile	Leu	Glu	Pro	Phe	695	Arg	Lys	Gln	Asn	Pro	700	Glu	Ile	Val
705	Ile	Tyr	710	Gln	Tyr	Met	Asp	Asp	715	Leu	Tyr	Val	Gly	Ser	720	Leu	Glu	Ile
			725						730						735			
Gly	Gln	His	740	Arg	Ala	Lys	Ile	Glu	745	Glu	Leu	Arg	Gly	His	750	Leu	Leu	Lys
Trp	Gly	Phe	755	Thr	Thr	Pro	Asp	Lys	760	Lys	His	Gln	Lys	Glu	765	Pro	Pro	Phe
Leu	Trp	Met	770	Gly	Tyr	Glu	Leu	His	775	Pro	Asp	Lys	Trp	Thr	780	Val	Gln	Pro
Ile	Lys	Leu	785	Pro	Glu	Lys	Asp	Ser	790	Trp	Thr	Val	Asn	Asp	795	Ile	Gln	Lys
Leu	Val	Gly	805	Lys	Leu	Asn	Trp	Ala	810	Ser	Gln	Ile	Tyr	Ala	815	Gly	Ile	Lys
Val	Arg	Gln	820	Leu	Cys	Lys	Leu	Leu	825	Arg	Gly	Thr	Lys	Ala	830	Leu	Thr	Glu
Val	Ile	Pro	835	Leu	Thr	Glu	Glu	Ala	840	Glu	Leu	Glu	Leu	Ala	845	Glu	Asn	Arg
Glu	Ile	Leu	850	Lys	Glu	Pro	Val	His	855	Gly	Val	Tyr	Tyr	Asp	860	Pro	Ser	Lys
Asp	Leu	Ile	865	Ala	Glu	Ile	Gln	Lys	870	Gln	Gly	Gln	Gly	Gln	875	Trp	Thr	Tyr
Gln	Ile	Tyr	885	Gln	Glu	Pro	Phe	Lys	890	Asn	Leu	Lys	Thr	Gly	895	Lys	Tyr	Ala
Arg	Met	Arg	900	Gly	Ala	His	Thr	Asn	905	Asp	Val	Lys	Gln	Leu	910	Thr	Glu	Ala
Val	Gln	Lys	915	Ile	Thr	Thr	Glu	Ser	920	Ile	Val	Ile	Trp	Gly	925	Lys	Thr	Pro
Lys	Phe	Lys	930	Leu	Pro	Ile	Gln	Lys	935	Glu	Thr	Trp	Glu	Thr	940	Trp	Trp	Thr
Glu	Tyr	Trp	945	Gln	Ala	Thr	Trp	Ile	950	Pro	Glu	Trp	Glu	Phe	955	Val	Asn	Thr
Pro	Pro	Leu	965	Val	Lys	Leu	Trp	Tyr	970	Gln	Leu	Glu	Lys	Glu	975	Pro	Ile	Val
Gly	Ala	Glu																